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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:16:02 ; Search time 38.2387 Seconds
(without alignments)
1359.585 Million cell updates/sec

Title: PCT-US03-05147-1
Perfect score: 964
Sequence: 1 MLQMAGQCSQNEYFDSLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	964	100.0	184	3	AAB08843	Aab08843 Amino aci
2	964	100.0	184	3	AAY94001	Aay94001 A human B
3	964	100.0	184	4	AAE09241	Aae09241 Human BCM
4	964	100.0	184	4	AAY71979	Aay71979 Human B c
5	964	100.0	184	4	AAB60698	Aab60698 Human BAF
6	964	100.0	184	4	AAE00506	Aae00506 Human B c
7	964	100.0	184	5	ABB81487	Abb81487 Human BCM
8	964	100.0	184	5	ABP54694	Abp54694 Metastati
9	964	100.0	184	5	AAE28961	Aae28961 Human B-c

10	964	100.0	184	6	AAE35216	Aae35216	Human	B-c
11	964	100.0	184	6	ADA49361	Ada49361	Human	BCM
12	964	100.0	184	6	ABP60552	Abp60552	Human	tum
13	964	100.0	184	6	ABP97717	Abp97717	Amino	aci
14	964	100.0	184	7	ADD67527	Add67527	Human	Lyl
15	958	99.4	184	6	ABR40082	Abr40082	Human	Gen
16	955	99.1	288	5	ABG95060	Abg95060	Human	tra
17	950	98.5	181	5	AAE15484	Aae15484	Human	B-c
18	719.5	74.6	157	4	AAB60700	Aab60700	Human	BAF
19	572	59.3	185	3	AAB08844	Aab08844	Amino	aci
20	572	59.3	185	4	AAV71980	Aay71980	Murine	B
21	572	59.3	185	5	AAE15490	Aae15490	Mouse	B c
22	323	33.5	58	5	AAE15501	Aae15501	Human	B c
23	311.5	32.3	117	5	AAE15491	Aae15491	Human-mur	
24	286.5	29.7	302	4	AAB60699	Aab60699	Mouse	IgG
25	286.5	29.7	302	4	AAE00507	Aae00507	Human	BCM
26	286	29.7	283	5	AAE15488	Aae15488	Human	BCM
27	284	29.5	51	5	AAE15485	Aae15485	Human	B-c
28	201	20.9	34	5	AAE15486	Aae15486	Human	B-c
29	201	20.9	34	6	ADA49366	Ada49366	Human	BCM
30	187	19.4	281	5	AAE15489	Aae15489	Mouse	BCM
31	158	16.4	42	6	ABJ38417	Abj38417	TALL-1	re
32	116.5	12.1	175	5	ABB78398	Abb78398	Amino	aci
33	116.5	12.1	175	5	AAE22244	Aae22244	Murine	BA
34	116.5	12.1	175	5	ABB81489	Abb81489	Mouse	Ztn
35	116.5	12.1	175	6	ABP97722	Abp97722	Amino	aci
36	106.5	11.0	185	5	AAE22266	Aae22266	Human	BAF
37	105.5	10.9	185	5	AAE22267	Aae22267	Human	BAF
38	104	10.8	21	5	AAE15487	Aae15487	Human	B-c
39	103.5	10.7	185	5	AAE22269	Aae22269	Human	BAF
40	100.5	10.4	185	5	AAE22271	Aae22271	Human	BAF
41	100	10.4	185	7	ADB90663	Adb90663	TALL-1R	g
42	99.5	10.3	185	5	AAE22268	Aae22268	Human	BAF
43	97.5	10.1	185	5	AAE22270	Aae22270	Human	BAF
44	94.5	9.8	185	5	AAE22242	Aae22242	Human	mat
45	93	9.6	184	5	ABB81483	Abb81483	Human	Ztn

ALIGNMENTS

RESULT 1

AAB08843

ID AAB08843 standard; peptide; 184 AA.

XX

AC AAB08843;

XX

DT 02-JAN-2001 (first entry)

XX

DE Amino acid sequence of human.

XX

KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;

KW anti-cell death gene; apoptosis; viral infection; inflammatory response;

KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT Domain 57. .77
 FT /note= "putative transmembrane domain"
 XX
 PN WO200050633-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 24-FEB-2000; 2000WO-US004925.
 XX
 PR 24-FEB-1999; 99US-0121485P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Seed B, Ting A;
 XX
 DR WPI; 2000-558405/51.
 XX
 PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression.
 XX
 PS Claim 32; Fig 7A; 53pp; English.
 XX
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is
 CC a necrosis factor (NF)-kB activator. The method of the invention is used
 CC to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQ MAGQCSQNEYFDSL LHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQ MAGQCSQNEYFDSL LHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 Qy 121 YTV EECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy      181 ISAR 184
      ||||
Db      181 ISAR 184

```

RESULT 2

AAAY94001

ID AAY94001 standard; protein; 184 AA.

XX

AC AAY94001;

XX

DT 20-OCT-2000 (first entry)

XX

DE A human BCMA protein, a B cell protein related to TACI.

XX

KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX

OS Homo sapiens.

XX

PN WO200040716-A2.

XX

PD 13-JUL-2000.

XX

PF 07-JAN-2000; 2000WO-US000396.

XX

PR 07-JAN-1999; 99US-00226533.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Gross JA, Xu W, Madden K, Yee DP;

XX

DR WPI; 2000-452538/39.

DR N-PSDB; AAA58559.

XX

PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX

PS Disclosure; Page 152; 175pp; English.

XX

CC The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell

CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL	60
Db	1	MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL	60
Qy	61	GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE	120
Db	61	GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE	120
Qy	121	YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180
Db	121	YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180
Qy	181	ISAR	184
Db	181	ISAR	184

RESULT 3

AAE09241

ID AAE09241 standard; protein; 184 AA.

XX

AC AAE09241;

XX

DT 19-NOV-2001 (first entry)

XX

DE Human BCMA protein.

XX

KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;

KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;

KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX

OS Homo sapiens.

XX

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PN      WO200160397-A1.
XX
PD      23-AUG-2001.
XX
PF      28-NOV-2000; 2000WO-US032378.
XX
PR      16-FEB-2000; 2000US-0182938P.
PR      22-AUG-2000; 2000US-0226986P.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ,  Dodge KH,  Grewal I,  Kim KJ,  Marsters SA,  Pitti RM;
XX      Yan M;
DR      WPI; 2001-541628/60.
DR      N-PSDB; AAD15902.
XX
PT      Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT      activity, for treating autoimmune disorders and cancer, comprises
PT      exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT      antagonists.
XX
PS      Example 2; Fig 2; 160pp; English.
XX
CC      The invention relates to methods of using one or more agonists or
CC      antagonists to modulate the activity of the members of TNF (tumour
CC      necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
CC      TACI or BCMA. The method is useful for treating pathological conditions
CC      or diseases associated with increased TALL-1 and APRIL expression or
CC      activity. TALL-1 and APRIL antagonists are used to block the interaction
CC      between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
CC      a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC      cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC      arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC      present sequence is human BCMA protein
XX
SQ      Sequence 184 AA;

Query Match          100.0%;  Score 964;  DB 4;  Length 184;
Best Local Similarity 100.0%;  Pred. No. 7.6e-95;
Matches 184;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTC 60
      |
Db      1  MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTC 60

Qy      61  GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
      |
Db      61  GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy      121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
      |
Db      121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy      181 ISAR 184
      ||||
Db      181 ISAR 184

```

RESULT 4

AA71979

ID AAY71979 standard; protein; 184 AA.

XX

AC AAY71979;

XX

DT 28-MAR-2001 (first entry)

XX

DE Human B cell maturation factor (BCMA) protein.

XX

KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;

KW Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1;

KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;

KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;

KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .62

FT /label= Extracellular_domain

XX

PN WO200068378-A1.

XX

PD 16-NOV-2000.

XX

PF 05-MAY-2000; 2000WO-US012266.

XX

PR 06-MAY-1999; 99US-0132892P.

PR 01-MAY-2000; 2000US-0201012P.

XX

PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX

PI Shu HS;

XX

DR WPI; 2001-016094/02.

DR N-PSDB; AAD02125.

XX

PT Isolated TALL-1 protein is used to identify compounds that regulate B

PT lymphocyte proliferation, used to treat B lymphocyte associated

PT autoimmune disorders.

XX

PS Claim 37; Page 104-105; 112pp; English.

XX

CC The present invention relates to Tumour necrosis factor (TNF) and ApoL-

CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,

CC proteins (including homologues), and their antibodies. The invention in

CC particular relates to methods for regulating the interaction between TALL

CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to

CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.

CC TALL-1 protein is useful for identifying compounds that regulate B

CC lymphocyte proliferation. It is also useful for treating B lymphocyte

CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA) protein.
 CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
 CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
 CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
 CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
 CC increases with B lymphocyte maturation
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL	60
Db	1	MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL	60
Qy	61	GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE	120
Db	61	GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE	120
Qy	121	YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180
Db	121	YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180
Qy	181	ISAR	184
Db	181	ISAR	184

RESULT 5

AAB60698

ID AAB60698 standard; protein; 184 AA.

XX

AC AAB60698;

XX

DT 22-MAY-2001 (first entry)

XX

DE Human BAFF receptor (BAFF-R).

XX

KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

KW immune-related disorder; B-cell growth inhibitor; BCMA;

KW B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

KW renal disorder; immunosuppressive disorder; HIV infection;

KW organ transplantation; antiinflammatory; systemic lupus erythematosus;

KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;

KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;

KW lymphoma; gene therapy; cancer; tumour.

XX

OS Homo sapiens.
 XX
 PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US022507.
 XX
 PR 17-AUG-1999; 99US-0149378P.
 PR 11-FEB-2000; 2000US-0181684P.
 PR 18-FEB-2000; 2000US-0183536P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTECH R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 PI Thompson J;
 XX
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 XX
 PS Claim 20; Fig 1; 59pp; English.
 XX
 CC The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAFF-R
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEYFDSLHACIPCQLRCSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

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      |||
Db      1 MLQMAGQCSQNEYFDSLHLHACIPCQLRCSSTNPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Qy      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
      |||
Db      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qy      121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
      |||
Db      121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy      181 ISAR 184
      |||
Db      181 ISAR 184

```

RESULT 6

AAE00506

ID AAE00506 standard; protein; 184 AA.

XX

AC AAE00506;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human B cell maturation protein (BCMA).

XX

KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;

KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;

KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;

KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;

KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;

KW organ transplantation; HIV; human immunodeficiency virus; TNF;

KW tumour necrosis factor; BCMA; B cell maturation protein.

XX

OS Homo sapiens.

XX

PN WO200124811-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027579.

XX

PR 06-OCT-1999; 99US-0157933P.

PR 11-FEB-2000; 2000US-0181807P.

PR 30-JUN-2000; 2000US-0215688P.

XX

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTTECH R & D SA.

XX

PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;

XX

DR WPI; 2001-266242/27.

DR N-PSDB; AAD03844.

XX

PT Treating a mammal for a condition associated with undesired cell

PT proliferation such as cancer or carcinoma, comprises administering a

PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)

PT antagonist.
 XX
 PS Claim 3; Fig 3A; 85pp; English.
 XX
 CC The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or carcinoma.
 CC The method involves administering a composition comprising A
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
 CC maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is human APRIL-R also referred as BCMA or BCM protein
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

 Qy 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

 Qy 181 ISAR 184
 ||||
 Db 181 ISAR 184

RESULT 7

ABB81487

ID ABB81487 standard; protein; 184 AA.

XX

AC ABB81487;

XX

DT 02-SEP-2002 (first entry)

XX

DE Human BCMA receptor related protein SEQ ID NO:7.

XX

KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;

KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;

KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200238766-A2.
 XX
 PD 16-MAY-2002.
 XX
 PF 05-NOV-2001; 2001WO-US047018.
 XX
 PR 07-NOV-2000; 2000US-0246449P.
 PR 20-DEC-2000; 2000US-0257131P.
 PR 28-JUN-2001; 2001US-0301715P.
 PR 29-AUG-2001; 2001US-0315565P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gross JA, Xu W, Henne RM, Grant FJ;
 XX
 DR WPI; 2002-508212/54.
 XX
 PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
 PT renal failure or renal disease and lymphoma.
 XX
 PS Disclosure; Page 135-136; 154pp; English.
 XX
 CC The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention

XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy    181 ISAR 184
          ||||
Db    181 ISAR 184
```

RESULT 8

ABP54694

ID ABP54694 standard; protein; 184 AA.

XX

AC ABP54694;

XX

DT 30-DEC-2002 (first entry)

XX

DE Metastatic colorectal cancer-associated polypeptide.

XX

KW Colorectal cancer; metastasis; differential expression; cytostatic;
KW diagnosis; gene therapy; vaccine.

XX

OS Homo sapiens.

XX

PN W0200268677-A2.

XX

PD 06-SEP-2002.

XX

PF 27-FEB-2002; 2002WO-US006001.

XX

PR 27-FEB-2001; 2001US-0272206P.

PR 02-APR-2001; 2001US-0281149P.

PR 17-APR-2001; 2001US-0284555P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX

PI Mack DH, Markowitz SD;

XX

DR WPI; 2002-698677/75.

DR N-PSDB; ABQ81560.

XX

FH Key Location/Qualifiers
 FT Region 1. .54
 FT /note= "Antigenic epitope"
 FT Domain 1. .48
 FT /note= "Extracellular domain"
 FT Region 8. .41
 FT /note= "Cysteine rich region"
 XX
 PN WO200266516-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 06-FEB-2002; 2002WO-US003500.
 XX
 PR 20-FEB-2001; 2001US-0270274P.
 PR 12-APR-2001; 2001US-0283447P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Kindsvogel W;
 XX
 DR WPI; 2002-723183/78.
 DR N-PSDB; AAD46410.
 XX
 PT B-cell maturation antigen and transmembrane activator and calcium-
 PT modulator and cyclophilin ligand-interactor, useful for treating
 PT disorders e.g. inflammation or lymphoma.
 XX
 PS Disclosure; Page 63; 67pp; English.
 XX
 CC The invention relates to the manufacture of a composition for inhibiting
 CC the proliferation of tumour cells. The method involves using an antibody
 CC component that binds both the B-cell maturation antigen (BCMA) and the
 CC transmembrane activator and calcium-modulator and cyclophilin ligand-
 CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
 CC for inhibiting proliferation of tumour cells, particularly inhibiting
 CC ZTNF4 activity in a mammal associated with increased endogenous antibody
 CC production or a disorder consisting of neoplasm, chronic lymphocytic
 CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
 CC lymphoproliferative disease or light chain gammopathy or inflammation
 CC e.g. asthma. The invention is also useful in gene therapy. The present is
 CC human BCMA protein
 XX
 SQ Sequence 184 AA;

 Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy 121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||
 Db 121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
 |||
 Db 181 ISAR 184

RESULT 10

AAE35216

ID AAE35216 standard; protein; 184 AA.

XX

AC AAE35216;

XX

DT 28-MAY-2003 (first entry)

XX

DE Human B-cell maturation receptor (BCMA) protein.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW B-cell maturation receptor; BCMA; receptor.

XX

OS Homo sapiens.

XX

PN WO200294852-A2.

XX

PD 28-NOV-2002.

XX

PF 20-MAY-2002; 2002WO-US015910.

XX

PR 24-MAY-2001; 2001US-0293343P.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Rixon MW, Gross JA;

XX

DR WPI; 2003-148455/14.

DR

N-PSDB; AAD53754.

XX

PT Transmembrane activator and calcium modulator and cyclophilin ligand-
 PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
 PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

XX

PS Disclosure; Col 100; 71pp; English.

XX

CC The invention relates to fusion proteins comprising transmembrane
 CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an
 CC immunoglobulin. The invention is used to manufacture a medicament for
 CC inhibiting the proliferation of tumour cells in a mammalian subject. The

CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human B-cell maturation receptor
CC (BCMA) protein used in the invention

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL	60
Db	1	MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL	60
Qy	61	GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE	120
Db	61	GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE	120
Qy	121	YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180
Db	121	YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS	180
Qy	181	ISAR	184
Db	181	ISAR	184

RESULT 11

ADA49361

ID ADA49361 standard; protein; 184 AA.

XX

AC ADA49361;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human BCMA protein.

XX

KW human; TALL-1; antagonist; immunosuppressive; antirheumatic;

KW antiinflammatory; antiarthritic; dermatological; antidiabetic;

KW neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;

KW vaccine; autoimmune disease; rheumatoid arthritis;

KW systemic lupus erythematosus; insulin dependent diabetes mellitus;

KW multiple sclerosis; myasthenia gravis; Grave's disease;

KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;

KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.

XX

OS Homo sapiens.

XX

PN WO2003035846-A2.

XX

PD 01-MAY-2003.

XX

PF 24-OCT-2002; 2002WO-US034376.

XX

PR 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348962P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX

PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX

PI Zhang G, Shu H, Liu Y, Xu L;

XX

DR WPI; 2003-403345/38.

DR N-PSDB; ADA49360.

XX

PT Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.

XX

PS Claim 62; Page 613; 618pp; English.

XX

CC The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting &bgr; strands
CC D and E that reduces the biological activity of the TALL- 1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. TC is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarteritis nodosa. The present sequence represents human BCMA.

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 7.6e-95;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

QY 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

QY 121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

QY 181 ISAR 184

Db |||||
 181 ISAR 184

RESULT 12

ABP60552

ID ABP60552 standard; protein; 184 AA.

XX

AC ABP60552;

XX

DT 28-MAR-2003 (first entry)

XX

DE Human tumour necrosis factor BCMA.

XX

KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;

KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;

KW antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic;

KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;

KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;

KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;

KW inflammatory disorder; proliferative disorder; single chain antibody;

KW antibody; human; BCMA; tumour necrosis factor.

XX

OS Homo sapiens.

XX

PN WO200294192-A2.

XX

PD 28-NOV-2002.

XX

PF 22-MAY-2002; 2002WO-US016106.

XX

PR 24-MAY-2001; 2001US-0293100P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM;

XX

DR WPI; 2003-156740/15.

XX

PT Novel isolated antibody that immunospecifically binds tumor necrosis

PT factor delta, useful for treating, preventing or ameliorating Non-

PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's

PT syndrome.

XX

PS Disclosure; Page 222; 225pp; English.

XX

CC The invention relates to a novel antibody or its fragment, which

CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).

CC The antibody of the invention has dermatological, immunosuppressive,

CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,

CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,

CC tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,

CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.

CC The antibody or its fragment are useful for treating, preventing or

CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in

CC human, disease or disorder such as autoimmune disease, and graft versus

CC host disease (GVHD). The autoimmune disease is systemic lupus

CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor BCMA

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

 Qy 121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

 Qy 181 ISAR 184
 ||||
 Db 181 ISAR 184

RESULT 13

ABP97717

ID ABP97717 standard; protein; 184 AA.

XX

AC ABP97717;

XX

DT 28-MAY-2003 (first entry)

XX

DE Amino acid sequence of human BCMA receptor.

XX

KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;

KW TALL-1; April; systemic lupus erythematosus; BCMA.

XX

OS Homo sapiens.

XX

PN WO2003014294-A2.

XX

PD 20-FEB-2003.

XX

PF 24-JUL-2002; 2002WO-US023487.

XX
 PR 03-AUG-2001; 2001US-0310114P.
 PR 30-APR-2002; 2002US-0377171P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dixit V, Grewal I, Ridgway J, Yan M;
 XX
 DR WPI; 2003-256560/25.
 DR N-PSDB; ABZ68871.
 XX
 PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.
 XX
 PS Disclosure; Fig 2; 153pp; English.
 XX
 CC The present sequence represents a human BCMA polypeptide. The
 CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
 CC preparing a composition for treating systemic lupus erythematosus
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 Qy 121 YTVEECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 YTVEECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 ||||
 Db 181 ISAR 184

RESULT 14

ADD67527

ID ADD67527 standard; protein; 184 AA.

XX

AC ADD67527;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human Lyl732P protein SEQ ID NO:4.

XX

KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;

KW vaccine; immunotherapy; cancer; multiple myeloma cell;
 KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003062401-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 22-JAN-2003; 2003WO-US002353.
 XX
 PR 22-JAN-2002; 2002US-00057475.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
 PI Carter L, Mcneill PD;
 XX
 DR WPI; 2003-598749/56.
 DR N-PSDB; ADD67526.
 XX
 PT New hematological malignancy-related genes and polypeptides, useful for
 PT screening anti-cancer agents, and generating antibodies or
 PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
 PT lymphocytic leukemia.
 XX
 PS Claim 9; SEQ ID NO 4; 307pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I), which is
 CC overexpressed in haematological malignancies, and which encodes a
 CC polypeptide or an immunogenic fragment of the polypeptide. Also
 CC described: (1) an isolated polypeptide; (2) an expression vector
 CC comprising (I) operably linked to an expression control sequence; (3) a
 CC host cell comprising an expression vector; (4) an isolated antibody that
 CC specifically binds to the polypeptide or its immunogenic fragment; and
 CC (5) immunoconjugates comprising the antibody above, or an antibody that
 CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
 CC by (I). (I) has cytostatic and immunostimulant activities, and can be
 CC used in vaccines and immunotherapy. The immunoconjugates are useful in
 CC the manufacture of a medicament, particularly as active ingredients in a
 CC composition for treating cancer, e.g. multiple myeloma cell, chronic
 CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
 CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
 CC The polynucleotide (I) or polypeptide can be used for screening anti-
 CC cancer agents, and generating antibodies or immunoconjugates for treating
 CC or preventing the above-mentioned diseases. The polynucleotide,
 CC polypeptide or antibody can be used for detecting, diagnosing or
 CC prognosticating the haematological malignancies described above. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 7; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 |||||
 Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy 121 YTVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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 Db 121 YTVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
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 Db 181 ISAR 184

RESULT 15

ABR40082

ID ABR40082 standard; protein; 184 AA.

XX

AC ABR40082;

XX

DT 27-JUN-2003 (first entry)

XX

DE Human Genoxit.

XX

KW Human; genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant;
 KW antidiabetic; hypotensive; ophthalmological; neuroprotective;
 KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
 KW Type III transmembrane protein; insulin resistance; atherosclerosis;
 KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;
 KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	1. .54
FT		/label= Extracellular_domain
FT	Misc-difference	3
FT		/label= Gln, Lys
FT	Domain	55. .77
FT		/label= Transmembrane_domain
FT	Domain	78. .184
FT		/label= Intracellular_domain

XX

PN WO2003013582-A1.

XX

PD 20-FEB-2003.

XX

PF 05-AUG-2002; 2002WO-IB003498.

XX

PR 06-AUG-2001; 2001US-0310754P.

XX

PA (GEST) GENSET SA.

XX

PI Lucas J, Dialynas D, Briggs K;

XX
 DR WPI; 2003-268160/26.
 DR N-PSDB; ACC00340.
 XX
 PT New use of agonist or antagonist of Genoxit activity for preventing or
 PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
 PT atherosclerosis.
 XX
 PS Disclosure; Page 32; 35pp; English.
 XX
 CC The present invention relates to the use of an agonist or antagonist of
 CC Genoxit activity for preventing or treating obesity. Genoxit is a member
 CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
 CC transmembrane protein. The agonists or antagonists of the invention are
 CC useful for treating or preventing obesity-related diseases or disorders,
 CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
 CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
 CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
 CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
 CC complications, e.g. microangiopathic lesions, ocular lesions,
 CC retinopathy, neuropathy and renal lesions
 XX
 SQ Sequence 184 AA;

Query Match 99.4%; Score 958; DB 6; Length 184;
 Best Local Similarity 99.5%; Pred. No. 3.3e-94;
 Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
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 Db 1 MLXMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 Qy 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 ||||
 Db 181 ISAR 184

Search completed: April 19, 2004, 13:20:57
 Job time : 40.2387 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:19:08 ; Search time 12.4938 Seconds
(without alignments)
760.310 Million cell updates/sec

Title: PCT-US03-05147-1
Perfect score: 964
Sequence: 1 MLQMAGQCSQNEYFDSLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	964	100.0	184	4	US-09-565-423-11	Sequence 11, Appl
2	572	59.3	185	4	US-09-565-423-17	Sequence 17, Appl
3	79.5	8.2	1009	2	US-08-357-642A-1	Sequence 1, Appli
4	79.5	8.2	1009	2	US-08-460-626-1	Sequence 1, Appli
5	78.5	8.1	293	2	US-08-810-572A-2	Sequence 2, Appli
6	78.5	8.1	293	4	US-09-290-333-2	Sequence 2, Appli
7	78.5	8.1	293	4	US-09-782-857A-2	Sequence 22, Appli
8	78.5	8.1	293	4	US-09-879-919-22	Sequence 22, Appli
9	78.5	8.1	293	4	US-09-848-295-4	Sequence 4, Appli
10	76	7.9	744	1	US-08-179-481-2	Sequence 2, Appli
11	75	7.8	857	1	US-07-717-331F-2	Sequence 2, Appli

12	71.5	7.4	835	4	US-09-489-039A-8740	Sequence 8740, Ap
13	71	7.4	333	4	US-09-328-352-6022	Sequence 6022, Ap
14	70.5	7.3	154	4	US-09-232-160-18	Sequence 18, Appl
15	69.5	7.2	166	2	US-08-810-572A-6	Sequence 6, Appli
16	69.5	7.2	166	4	US-09-290-333-6	Sequence 6, Appli
17	69.5	7.2	166	4	US-09-782-857A-6	Sequence 6, Appli
18	69.5	7.2	217	4	US-09-252-991A-30641	Sequence 30641, A
19	69.5	7.2	224	4	US-09-465-901-30	Sequence 30, Appl
20	69.5	7.2	353	4	US-09-328-352-5429	Sequence 5429, Ap
21	69.5	7.2	942	4	US-09-695-481-2	Sequence 2, Appli
22	69.5	7.2	1043	4	US-09-695-481-6	Sequence 6, Appli
23	69.5	7.2	1180	3	US-08-660-148-2	Sequence 2, Appli
24	69.5	7.2	1212	3	US-08-660-148-5	Sequence 5, Appli
25	69.5	7.2	1212	4	US-09-695-481-7	Sequence 7, Appli
26	69.5	7.2	1706	2	US-08-459-568-2	Sequence 2, Appli
27	69.5	7.2	1706	2	US-08-399-411-2	Sequence 2, Appli
28	69.5	7.2	1706	3	US-08-516-859A-2	Sequence 2, Appli
29	69.5	7.2	1706	4	US-09-586-472-2	Sequence 2, Appli
30	69.5	7.2	1706	4	US-09-528-706-2	Sequence 2, Appli
31	69.5	7.2	2496	3	US-09-125-028-2	Sequence 2, Appli
32	69.5	7.2	2958	3	US-08-894-344C-2	Sequence 2, Appli
33	69	7.2	324	2	US-08-579-940-7	Sequence 7, Appli
34	69	7.2	445	1	US-08-353-400-33	Sequence 33, Appl
35	69	7.2	447	6	5455030-1	Patent No. 5455030
36	69	7.2	464	1	US-08-353-400-36	Sequence 36, Appl
37	69	7.2	599	1	US-08-442-542-18	Sequence 18, Appl
38	69	7.2	599	3	US-08-765-469-18	Sequence 18, Appl
39	68.5	7.1	228	4	US-09-107-532A-3896	Sequence 3896, Ap
40	68.5	7.1	295	3	US-08-651-136C-8	Sequence 8, Appli
41	68.5	7.1	295	4	US-09-229-911A-8	Sequence 8, Appli
42	68.5	7.1	877	1	US-08-072-574-12	Sequence 12, Appl
43	68.5	7.1	877	1	US-08-486-270-12	Sequence 12, Appl
44	68.5	7.1	877	3	US-08-367-264-12	Sequence 12, Appl
45	68.5	7.1	877	4	US-09-153-757-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-565-423-11

; Sequence 11, Application US/09565423

; Patent No. 6475987

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/09/565,423

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 100.0%; Score 964; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.5e-104;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
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Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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Db    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy    181 ISAR 184
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Db    181 ISAR 184
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RESULT 2

US-09-565-423-17

; Sequence 17, Application US/09565423

; Patent No. 6475987

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/09/565,423

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-565-423-17

Query Match 59.3%; Score 572; DB 4; Length 185;
Best Local Similarity 62.6%; Pred. No. 2.2e-58;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

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Qy      4 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
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Db      1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYYTVLWIFLGLT 58
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Qy 64 LIISLAVFVLMFLLRKISSEPLKDEFKN-----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
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 Db 59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSQQLDKADTELTRIRAGDDRIFPRSL 118

Qy 120 EYTVVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 |||||:|||| |||| ||||| ||||| || | | : | || | :
 Db 119 EYTVVEECTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTGDYKSSVPTALQSVMMGM 178

Qy 178 EKSISAR 184
 || |
 Db 179 EKPTHTR 185

RESULT 3

US-08-357-642A-1

; Sequence 1, Application US/08357642A

; Patent No. 5837524

; GENERAL INFORMATION:

; APPLICANT: Sima Lev

; APPLICANT: Joseph Schlessinger

; TITLE OF INVENTION: PYK2 RELATED PRODUCTS

; TITLE OF INVENTION: AND METHODS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/357,642A

; FILING DATE: December 15, 1994

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/070

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1009

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-357-642A-1

Query Match 8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 3.8;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

Qy 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLETVVEECTCEDCIKSKPKV 138
:| || | | ||| | | | | :| |:| : | : ::
Db 249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305

Qy 139 DSDHCFPLPAMEEGATIL 156
| | || ||| :|
Db 306 RSIRCLPL---EEGQAVL 320

RESULT 4

US-08-460-626-1

; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-626-1
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Query Match      8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 3.8;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;
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Qy      88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
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Db      249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305

Qy      139 DSDHCFPLPAMEEGATIL 156
      | | ||  ||| :|
Db      306 RSIRCLPL---EEGQAVL 320
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RESULT 5

US-08-810-572A-2

; Sequence 2, Application US/08810572A

; Patent No. 5969102

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; APPLICANT: von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/810,572A

; FILING DATE: 28-FEB-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1340-1-007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 293 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
US-08-810-572A-2
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Query Match          8.1%; Score 78.5; DB 2; Length 293;
Best Local Similarity 19.9%; Pred. No. 0.86;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;
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QY      8 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
      | : :|:| || |: |: |: : || :| : :| : :| |: : |
Db     34 CPEEQYWDPLLGTCSCKTICNHQS-QRTCAAFCSRSLSCRKEQGKFYDHLRLDCISCASI 92

QY     66 I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS----- 107
      | | | | | | | | | | | | | | | | | | | | | |
Db     93 CGQHPKQCA YFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151

QY    108 ---RTGDEIILPRG-----LEVTVEECTCEDCIKSKP-----KVD 139
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Db    152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209

QY    140 SDHCFPLPAMEEGATILVTTKTNDYC 165
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Db    210 QDH-----AMEAGSPVSTSPPEPVETC 230
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RESULT 6

US-09-290-333-2

; Sequence 2, Application US/09290333

; Patent No. 6316222

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS

OF USE

; THEREOF

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/290,333
;           FILING DATE: 12-Apr-1999
;           CLASSIFICATION: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;           NAME: Jackson Esq., David A.
;           REGISTRATION NUMBER: 26,742
;           REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
;
; TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 201-487-5800
;           TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 2:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 293 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;
;           MOLECULE TYPE: protein
;           HYPOTHETICAL: NO
;           FRAGMENT TYPE: N-terminal
;           ORIGINAL SOURCE:
;               ORGANISM: Homo sapiens
;           SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

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Query Match          8.1%;  Score 78.5;  DB 4;  Length 293;
Best Local Similarity 19.9%;  Pred. No. 0.86;
Matches 41;  Conservative 35;  Mismatches 73;  Indels 57;  Gaps 10;

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Qy      8 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
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Db     34 CP EEQYWDPLLGT C MSCKTICNHQS-QRTCAAFCSRSLSCRKEQGKFYDHL LRDCISCASI 92

Qy     66 I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS----- 107
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Db     93 CGQHPKQ CAYFCENKLRSPVNLPPELRRQRSGEVENNSD NSGR-YQGLEHRGSEASPALP 151

Qy    108 ---RTGDEIILPRG-----LEYTVEECTCEDCIKSKP-----KVD 139
      : |:: | | | | | | | | | | | | | | | | | | | | | |
Db    152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209

Qy    140 SDHCFPLPAMEEGATILVTTKTNDYC 165
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Db    210 QDH-----AMEAGSPVSTSPFPVETC 230

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RESULT 7

US-09-782-857A-2

; Sequence 2, Application US/09782857A

; Patent No. 6500428

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS


```

;                                CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS
OF USE
;                                THEREOF
;    NUMBER OF SEQUENCES: 10
;    CORRESPONDENCE ADDRESS:
;        ADDRESSEE: David A. Jackson, Esq.
;        STREET: 411 Hackensack Ave, Continental Plaza, 4th
;            Floor
;        CITY: Hackensack
;        STATE: New Jersey
;        COUNTRY: USA
;        ZIP: 07601
;    COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/782,857A
;        FILING DATE: 14-Feb-2001
;        CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 08/810,572
;        FILING DATE: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;        NAME: Jackson Esq., David A.
;        REGISTRATION NUMBER: 26,742
;        REFERENCE/DOCKET NUMBER: 1340-1-007
;    TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 201-487-5800
;        TELEFAX: 201-343-1684
;    INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 293 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: NO
;        FRAGMENT TYPE: N-terminal
;        ORIGINAL SOURCE:
;            ORGANISM: Homo sapiens
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

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Query Match          8.1%;  Score 78.5;  DB 4;  Length 293;
Best Local Similarity 19.9%;  Pred. No. 0.86;
Matches 41;  Conservative 35;  Mismatches 73;  Indels 57;  Gaps 10;

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Qy      8 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCGLGLSLI 65
      | : : | : | | | : | : | : | : | : | : | : | : |
Db      34 CP EEQYWD PLLGTCMSCKTICNHQS-QRTCAAFCSRSLSCRKEQGKFYDHLRLDCISCASI 92

Qy      66 I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
      | | | | | | | | | | | | | | | | | | | | | |
Db      93 CGQHPKQ CAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151

```

```

Qy      108 ---RTGDEIILPRG-----LEYTVEECTCEDCIKSKP-----KVD 139
          : |:: |                               |:  : |::  :|:|  |
Db      152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209

Qy      140 SDHCFPLPAMEEGATILVTTKTNDYC 165
          ||      ||| |:  :  :  : |
Db      210 QDH-----AMEAGSPVSTSPEPVETC 230

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RESULT 8

US-09-879-919-22

; Sequence 22, Application US/09879919

; Patent No. 6541224

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang, et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon

; FILE REFERENCE: PF253P1

; CURRENT APPLICATION NUMBER: US/09/879,919

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,978

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/254,875

; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: 60/241,952

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/211,537

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 08/815,783

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: 60/016,812

; PRIOR FILING DATE: 1996-03-14

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-879-919-22

Query Match 8.1%; Score 78.5; DB 4; Length 293;

Best Local Similarity 19.9%; Pred. No. 0.86;

Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

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Qy      8 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
          | : :|:| || |: |: |:  : || :| :  :| : :| |:  : |
Db      34 CP EEQYWDPLLGT C MSCKTICNHQS-QRTCAAFCSRSLSCRKEQGKFYDHLRLDCISCASI 92

Qy      66 I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
          | |      |           ||: | :::  |:| |:  : | |
Db      93 CGQHPKQ CAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151

Qy      108 ---RTGDEIILPRG-----LEYTVEECTCEDCIKSKP-----KVD 139
          : |:: |                               |:  : |::  :|:|  |

```

```

Db      152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
Qy      140 SDHCFPLPAMEEGATILVTTKTNDYC 165
          ||      ||| |: : : : : |
Db      210 QDH-----AMEAGSPVSTSPEPVETC 230

```

RESULT 9

```

US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; TITLE OF INVENTION: Thereon
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4

```

```

Query Match          8.1%; Score 78.5; DB 4; Length 293;
Best Local Similarity 19.9%; Pred. No. 0.86;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

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Qy      8 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
          | : :|:| || |: |: |: : || :| : :| |: :|
Db      34 CPEEQYWDPLLGTCTMCKTICNHQS-QRTCAAFCSRSLSCRKEQGKFYDHLRDCISCASI 92

Qy      66 I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
          ||      |      ||: | ::: |:| |: : | |
Db      93 CGQHPKQCAYFCENKLRSPVNLPPELRRQSRGEVENNSDNSGR-YQGLEHRGSEASPALP 151

Qy      108 ---RTGDEIILPRG-----LEYTVEECTCEDCIKSKP-----KVD 139
          : |: : |      |: : |:|: :|:| |
Db      152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209

Qy      140 SDHCFPLPAMEEGATILVTTKTNDYC 165
          ||      ||| |: : : : : |
Db      210 QDH-----AMEAGSPVSTSPEPVETC 230

```

RESULT 10

```

US-08-179-481-2
; Sequence 2, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARRAWAY, KERMIT L.
; APPLICANT: CAROTHERS CARRAWAY, CORALIE A.

```

```

; APPLICANT: FREGIEN, NEVIS L.
; TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,481
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,521
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-179-481-2

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Query Match          7.9%; Score 76; DB 1; Length 744;
Best Local Similarity 22.1%; Pred. No. 6.3;
Matches 34; Conservative 29; Mismatches 57; Indels 34; Gaps 6;

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Qy      4 MAGQCSQNEYFDSLHLHACIPCQLRCSSNTPPLTCQRYC-----NASVTNSVKGT 52
      : |: |: | : :: | || |:| | : | :| : |
Db      49 LEGRTAQTDSANATNFIAFAAQYNTSSLKSPITVQWFLEPNDTIRVVHNNQTVAFNTSDT 108

Qy      53 NAI-LWTCLGLSLI-----ISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLG 98
      : :: |: || ::::| | :| || | :|::| |||
Db      109 EDLPVFNATGVLLIQNGSQVSANFDGTVTISVIALSNILHASS--LSEERYNHTKGLLG 166

Qy      99 MANIDLEKSRTGDEIILPRGLETVVEECTCEDCI 132
      : | : | |: :| | |: | | : :
Db      167 VWNDNPE-----DDFRMPNG--STIPSNTSEETL 193

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RESULT 11
US-07-717-331F-2

```

```

; Sequence 2, Application US/07717331F
; Patent No. 5484905
; GENERAL INFORMATION:
;   APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
;   APPLICANT: Stein
;   TITLE OF INVENTION: A Receptor Protein Kinase Gene
;   TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Yahwak & Associates
;     STREET: 25 Skytop Drive
;     CITY: Trumbull
;     STATE: Connecticut
;     COUNTRY: USA
;     ZIP: 06611
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy Disk
;     COMPUTER: Macintosh
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: Microsoft Word
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/717,331F
;     FILING DATE: June 19th 1991
;     CLASSIFICATION: 800
;   ATTORNEY/AGENT INFORMATION:
;     NAME: George M. Yahwak
;     REGISTRATION NUMBER: 26,824
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (203)268-1951
;     TELEFAX: (203)268-1951
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 857 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-07-717-331F-2

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Query Match          7.8%; Score 75; DB 1; Length 857;
Best Local Similarity 17.6%; Pred. No. 10;
Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

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Qy      24 CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT----- 58
      |: || |:      | : || : |   |: ::||
Db      380 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTTERLEDIRNYATDAIDGQDLYVRLAA 434

Qy      59 -----CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
      : |:: :|: : ::|| |      | : |   : : :||   :
Db      435 ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WKRKQKRAKASAI SIANTQRNQ 487

Qy      107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDS DHCF-----PLPAMEEGATILVTTKT 161
      : :|::|      || :   :: |   || ||   |:: |:
Db      488 NLPNMNEMVL-----SSKREFSGEYKFEELELPLIEME---TVVKATEN 527

Qy      162 NDYCKSL 168
      | |
Db      528 FSSCNKL 534

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RESULT 12

US-09-489-039A-8740

; Sequence 8740, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8740

; LENGTH: 835

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8740

Query Match 7.4%; Score 71.5; DB 4; Length 835;

Best Local Similarity 21.0%; Pred. No. 25;

Matches 56; Conservative 36; Mismatches 80; Indels 95; Gaps 14;

```

Qy      1 MLQMAGQCSQNE-----YFDSLHACIP---CQL-----RCSSNTPPLT 36
      |: ||| : ||           | ::| ||:   |::           | |
Db      199 MILMAGFTAGNEKGELVVLGRNGSDYSAAVLAACLRADCCEIWTDVDGVYTC DPRQVP-- 256

Qy      37 CQRYCNASVTNSVKGTNAILWTCLGLSL-----IISLAVFVLMFLLRKISSEPL----- 85
      :| : |: | : : | : | :| | : |:: :
Db      257 -----DARLLKSMSYQEAMELSYFGAKVLHPRTIAPIAQFQIPCLIKNTGNPQAPGTLIG 311

Qy      86 --KDE-----FKNTGSGLLGM-----ANIDLEKSRTGDEIIL--PRGLEY 121
      :||           | :| ||: ||   | :   || | :||   ||
Db      312 ASRDEDDLVPVKGISNLNMMAMFNVSGPGMKGMVGMMAARVFATMSRAGISVVLITQSSEY 371

Qy      122 TVEECTCE-DCIKSKPKVDS DHCF-----PLPAMEEGATILVTTKTNDYCKSLP--- 169
      :: | : || ::| :: :   || || | | |   | :|
Db      372 SISFCVPQSDCARAKRAMEDEFYLELKEGLLEPLAIMERLAIISV---VGDGMRTLRLGIS 428

Qy      170 ----AALSATEI-----EKSIS 182
      |||: |           |::||
Db      429 AKFFAALARANINIVAIAQGSSERSIS 455

```

RESULT 13

US-09-328-352-6022

; Sequence 6022, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

```
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6022
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-6022
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RESULT 14

Query Match 7.3%; Score 70.5; DB 4; Length 154;
Best Local Similarity 25.2%; Pred. No. 2.9;
Matches 30; Conservative 16; Mismatches 52; Indels 21; Gaps 6;

```

Db          23 YADDCLAQCGKDKCSYCCDGTTPYCCSY--AYIGNILSGT-AIAGIVFGIVFIMGVIAG 79
Qy          68 LAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC 126
           :|: : | :           : | |:| :|: | | | | :|: :| |
Db          80 IAICICMCM-----KNHRATRVGILRTTHINTVSSYPGPP---PYGHDHEMEYC 125

```

RESULT 15

US-08-810-572A-6

; Sequence 6, Application US/08810572A

; Patent No. 5969102

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; APPLICANT: von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/810,572A

; FILING DATE: 28-FEB-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1340-1-007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 166 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

US-08-810-572A-6

Query Match

7.2%; Score 69.5; DB 2; Length 166;

Best Local Similarity 25.0%; Pred. No. 4.2;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

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Qy      8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
      | : :|:| || |: |: |: : || :| :      :| : :| |: :|
Db     34 CP EEQYWDPLLGT C MSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
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Search completed: April 19, 2004, 13:24:20
Job time : 13.4938 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:18:32 ; Search time 10.2222 Seconds
(without alignments)
1731.447 Million cell updates/sec

Title: PCT-US03-05147-1
Perfect score: 964
Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	964	100.0	184	2	S43486	B-cell maturation
2	88.5	9.2	217	2	C97344	amino acid ABC tra
3	86.5	9.0	858	2	T08881	prominin - mouse
4	83.5	8.7	1998	2	T13009	hypothetical prote
5	82	8.5	1009	2	A57434	protein-tyrosine k
6	81.5	8.5	2233	2	T28669	surface protein 51
7	81	8.4	773	2	D89010	protein R08F11.7 [
8	79.5	8.2	1009	2	S60248	protein-tyrosine k
9	79.5	8.2	1299	2	T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	2	D64469	potassium channel
11	78	8.1	841	2	JC5894	killer cell inhibi
12	77.5	8.0	738	2	D86345	hypothetical prote
13	77.5	8.0	968	2	T01733	hypothetical prote

14	77	8.0	522	2	T45824	hypothetical prote
15	77	8.0	539	2	F72288	methyl-accepting c
16	76.5	7.9	357	2	T21152	hypothetical prote
17	76.5	7.9	1404	2	T19277	hypothetical prote
18	76	7.9	744	2	A43353	ascites sialoglyco
19	76	7.9	748	2	T47250	complex I intermed
20	75.5	7.8	638	2	T41478	probable transcrip
21	75	7.8	450	2	B97297	hydrogenase chain
22	75	7.8	857	1	A41369	S-receptor kinase
23	74.5	7.7	384	2	S45592	ERD1 protein - yea
24	74.5	7.7	1101	2	T16840	hypothetical prote
25	74	7.7	377	2	JC7535	chitinase (EC 3.2.
26	73.5	7.6	307	2	B95099	membrane protein [
27	73.5	7.6	307	2	A97967	conserved hypothet
28	73	7.6	304	2	A89882	hypothetical prote
29	73	7.6	679	2	B96599	protein F20N2.12 [
30	73	7.6	733	1	A46373	probable serine/th
31	72.5	7.5	243	2	T31144	hypothetical prote
32	72.5	7.5	408	2	B84518	hypothetical prote
33	72	7.5	416	2	S75097	hypothetical prote
34	72	7.5	855	2	T10665	hypothetical prote
35	71.5	7.4	105	2	T10350	hypothetical prote
36	71.5	7.4	627	2	B71709	hypothetical prote
37	71	7.4	227	2	F72334	conserved hypothet
38	71	7.4	414	2	G71331	probable cell divi
39	71	7.4	473	2	AF1207	ABC transporters (
40	71	7.4	480	2	G88690	protein F41H10.1 [
41	71	7.4	500	2	T10543	hypothetical prote
42	71	7.4	660	2	T02768	spike glycoprotein
43	70.5	7.3	188	2	H82933	hypothetical prote
44	70.5	7.3	412	2	T24023	hypothetical prote
45	70.5	7.3	424	2	T14525	S-locus-specific g

ALIGNMENTS

RESULT 1

S43486

B-cell maturation factor - human

N;Alternate names: BCM protein; BCMA protein; BEL protein

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000

C;Accession: S43486; S31208; S36661

R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.

Nucleic Acids Res. 22, 1147-1154, 1994

A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.

A;Reference number: S43486; MUID:94218235; PMID:8165126

A;Accession: S43486

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-184 <LAA>

A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245

R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.

EMBO J. 11, 3897-3904, 1992

A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.
 A;Reference number: S31208; MUID:93010984; PMID:1396583
 A;Accession: S31208
 A;Molecule type: mRNA
 A;Residues: 1-184 <LA2>
 A;Cross-references: EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:g29408
 A;Accession: S36661
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 4-184 <LA3>
 A;Cross-references: EMBL:Z14955
 C;Genetics:
 A;Gene: GDB:BCMA
 A;Cross-references: GDB:135977; OMIM:109545
 A;Map position: 16p13.1-16p13.1
 A;Introns: 44/1; 93/1
 C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 964; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.1e-81;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
        |||
Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        |||
Db      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy      121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
        |||
Db      121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy      181 ISAR 184
        ||||
Db      181 ISAR 184
  
```

RESULT 2

C97344

amino acid ABC transporter, permease component CAC3619 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

C;Accession: C97344

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: C97344

A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-217 <KUR>
 A;Cross-references: GB:AE001437; PIDN:AAK81542.1; PID:g15026719; GSPDB:GN00168
 A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC3619
 C;Superfamily: histidine permease protein M

Query Match 9.2%; Score 88.5; DB 2; Length 217;
 Best Local Similarity 24.8%; Pred. No. 0.99;
 Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

```

Qy      16 SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL 62
          | |: || | : | || | : ||| | | | | |
Db      4  SSLNKVIPVLLDGRITLLLTCSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT 63

Qy      63 SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
          |:: | |: | || |: | |: | | | | | | |
Db      64 PLLLQLYVYYYGLPFLSDKLTMTMPKAAILGLSLNSGAYIAEIIIRGGILADNGQFEASK 123

Qy     109 -----TGDEIILPRGLEYTVEEC-----TCEDCI-KSKPKVDS DH 142
          | |||: : : | | | | | | | | |
Db     124 ALGLTYGQTMKRIILPQAIRVVI PPCGNEFIAMIKDTSLSVITMEELLRKAQLLVSSSG 183

Qy     143 CFPLPAMEEGA--TILVTTKTNDYCKSLPAALSATEIEKSI 182
          | : | || | | : | || | |
Db     184 DAVTPYLFAGIFYLILTTIFTGIFSK-----IEKKLS 215
  
```

RESULT 3

T08881

prominin - mouse

C;Species: Mus musculus (house mouse)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: T08881

R;Weigmann, A.; Corbeil, D.; Hellwig, A.; Huttner, W.B.

Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997

A;Title: Prominin, a novel microvilli-specific polytopic membrane protein of the apical surface of epithelial cells, is targeted to plasmalemmal protrusions of non-epithelial cells.

A;Reference number: Z16512; MUID:98024147; PMID:9356465

A;Accession: T08881

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-858 <WEI>

A;Cross-references: EMBL:AF026269; NID:g2559003; PIDN:AAB86715.1; PID:g2559004

A;Experimental source: kidney

C;Keywords: glycoprotein; membrane protein

Query Match 9.0%; Score 86.5; DB 2; Length 858;
 Best Local Similarity 22.7%; Pred. No. 6;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

```

Qy      18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
          | | | || | : | : | | |||||: : | :
Db     117 LVGCFFCMCRC-----CNK-CGGEMHQKQKQKQAPCRRKCLGLSLLVICLLMSLGIIY 167
  
```

Qy	78	RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYYTVEECTCE----	129
		::: : : : : : :	
Db	168	GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA	218
Qy	130	----DCIKS-----KPKVDS DHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL--	172
		: : : : :	
Db	219	FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS	271
Qy	173	---SATEIEKSISA	183
		: : : : :	
Db	272	LQDAATQNTNLSS	285

RESULT 4

T13009

hypothetical protein T24C20.80 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text change 24-Nov-1999

C;Accession: T13009

R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.;

Artiguenave, F.; Saurin, W.; Weissenbach, J.; Mewes, H.W.; Mayer, K.F.X.:

Lemcke, K.; Schueller, C.; Quetier, F.; Salanoubat, M.

submitted to the Protein Sequence Database, July 1999

A;Reference number: Z17586

A;Accession: T13009

A;Molecule type: DNA

A;Residues: 1-1998 <CHO>

A;Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80

A; Experimental source: cultivar Columbia; BAC clone T24C20

C; Genetics:

A; Gene: ATSP:T24C20.80

```
A;Map position: 3
```

A; Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/2; 1461/3; 1791/3; 1867/1; 1914/3

C;Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80

Query Match 8.7%; Score 83.5; DB 2; Length 1998;

Best Local Similarity 29.4%; Pred. No. 27;

Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

```

Qy          38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS  94
      :|||:|  ||  || ::  |                               |: | :| ||:|  |
Db          1089 ERYCSA---NSALGTPSM---C-----SSTGPFQDSEFENFSLGP 1122

Qy          95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDS DHCFPLPAM 149
      |: ::::|: || ||      ||: :  | :|      ||      |: || | | |
Db          1123 SLVKLSSLDM--SRLGD-----RGIHFFDEGGSCNGRSSAPGLNTGNVNIDMCGDL--M 1173

Qy          150 EEGATI 155
      : ||||
Db          1174 DGGATI 1179

```

RESULT 5

A57434

protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat

N;Alternate names: cell adhesion kinase-beta

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 04-Feb-2000
 C;Accession: A57434
 R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
 J. Biol. Chem. 270, 21206-21219, 1995
 A;Title: Cloning and characterization of cell adhesion kinase beta, a novel
 protein-tyrosine kinase of the focal adhesion kinase subfamily.
 A;Reference number: A57434; MUID:95403356; PMID:7673154
 A;Accession: A57434
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1009 <SAS>
 A;Cross-references: GB:D45854; NID:g1000679; PIDN:BAA08290.1; PID:d1008885;
 PID:g1000680
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
 kinase homology
 C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F;423-686/Domain: protein kinase homology <KIN>
 F;431-439/Region: protein kinase ATP-binding motif

Query Match 8.5%; Score 82; DB 2; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 18;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
 :| || | | ||| | | | | :| |:| : | : :
 Db 249 KFFNT---LAGFANIDQETRYCELIQGWNTVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
 QY 139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
 | | || : ||| :: ||: ||:
 Db 306 RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSSLAEAEENMADLIDGYCR 353

RESULT 6

T28669

surface protein 51C - Paramecium tetraurelia

C;Species: Paramecium tetraurelia

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999

C;Accession: T28669

R;Nielsen, E.; You, Y.; Forney, J.

J. Mol. Biol. 222, 835-841, 1991

A;Title: Cysteine residue periodicity is a conserved structural feature of
 variable surface proteins from Paramecium tetraurelia.

A;Reference number: Z20504; MUID:92106337; PMID:1762150

A;Accession: T28669

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2233 <NIE>

A;Cross-references: EMBL:M65164; NID:g159974; PID:g159975; PIDN:AAA61740.1

C;Genetics:

A;Genetic code: SGC5

Query Match 8.5%; Score 81.5; DB 2; Length 2233;
 Best Local Similarity 25.1%; Pred. No. 46;
 Matches 43; Conservative 17; Mismatches 58; Indels 53; Gaps 10;

QY 6 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA-SVTNSVKGTNAILWLTCLGLSL 64

```

      | | | :      |      | |      | | | : : | |      | : | |
Db      520 GSCYQKQ-----CSAASQDNTTHAQCEYLPACTLSNTKKG-----CIDLPL 561
QY      65 IISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDL----EKSRTGDEIILPRGLE 120
      |      | : | : | : |      | |      : | :      : | |      :
Db      562 TCSA-----LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-----D 603
QY      121 YTVEECTC----EDCIKSKPKVSDSDHCFPLPAMEEGATI-----LVTTKTN 162
      | | | |      : | :      | | | |      | |      : | | |
Db      604 YTVELCEAYKPSSNCV---PNGTKKGCMELAAKCESRTIKEQCDVAGTKTN 651

```

RESULT 7

D89010

protein R08F11.7 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002

C;Accession: D89010

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ for a list of authors

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999

A;Accession: D89010

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-773 <STO>

A;Cross-references: GB:chr_V; PIDN:AAB54249.1; PID:g2088832; GSPDB:GN00023; CESP:R08F11.7

A;Note: Similar to peroxidase

C;Genetics:

A;Gene: R08F11.7

A;Map position: 5

C;Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 8.4%; Score 81; DB 2; Length 773;

Best Local Similarity 21.7%; Pred. No. 17;

Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6;

```

QY      23 PCQLRCSSNTPPLTCQ-----RYCN----ASVTNSVKGTNAILWTCL---GLSL 64
      | :      : | | : |      | | |      : | | |      : | |      | |
Db      184 PPKSNATCQGPPKSCSDPVHDIRSITGYCNNRGKPTQANSVTAIRRLGTTSTYDGLQA 243
QY      65 IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLE YTV 123
      | : : |      : : | | | |      | :      : : : :      | | : |
Db      244 IRNTSVTGSPLPSTRLLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG 303
QY      124 EECTCEDCIKSKPKVSDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----TE 176
      | | | |      | : | | : | |      : : | | | |      | :      | :
Db      304 SSLNCTSC--SSPTTISTNCAPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ 361
QY      177 IEKS 180
      | : :

```


Db

362 IDQN 365

RESULT 8

S60248

protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - human

N;Alternate names: cell adhesion kinase-beta

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1996 #sequence_revision 27-Feb-1997 #text_change 17-Nov-2000

C;Accession: S60248; G02330; B57434

R;Lev, S.; Moreno, H.; Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.;
Plowman, G.D.; Rudy, B.; Schlessinger, J.

Nature 376, 737-745, 1995

A;Title: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of
ion channel and MAP kinase functions.

A;Reference number: S60248; MUID:95379967; PMID:7544443

A;Accession: S60248

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1009 <LEV>

A;Cross-references: EMBL:U33284; NID:g988304; PIDN:AAC50203.1; PID:g988305

R;Sasaki, T.; Nagura, K.; Sasaki, H.

submitted to the EMBL Data Library, December 1995

A;Reference number: H01067

A;Accession: G02330

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-22,'G',24-434,'L',436-1009 <SAS>

A;Cross-references: EMBL:U43522; NID:g1165218; PIDN:AAC05330.1; PID:g1165219

R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobiooka, H.; Kotani, K.; Sasaki, T.

J. Biol. Chem. 270, 21206-21219, 1995

A;Title: Cloning and characterization of cell adhesion kinase beta, a novel
protein-tyrosine kinase of the focal adhesion kinase subfamily.

A;Reference number: A57434; MUID:95403356; PMID:7673154

A;Accession: B57434

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-22,'G',24-150 <SA2>

A;Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884;
PID:g1000677

C;Genetics:

A;Gene: CAKbeta

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
kinase homology

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;423-686/Domain: protein kinase homology <KIN>

F;431-439/Region: protein kinase ATP-binding motif

Query Match 8.2%; Score 79.5; DB 2; Length 1009;

Best Local Similarity 32.1%; Pred. No. 31;

Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

Qy 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138

:| || | | |||| | | | | :| |:: : | : :

Db 249 KFFNT---LAGFANIDQETRYCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305

Qy 139 DSDHCFPLPAMEEGATIL 156

| | || ||| :|
Db 306 RSIRCLPL---EEGQAVL 320

RESULT 9

T43251

furin (EC 3.4.21.75) - fall armyworm

N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serine proteinase PACE

C;Species: Spodoptera frugiperda (fall armyworm)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C;Accession: T43251

R;Cieplik, M.; Klenk, H.

submitted to the EMBL Data Library, January 1996

A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiperda (Sf9) cells.

A;Reference number: Z22368

A;Accession: T43251

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1299 <CIE>

A;Cross-references: EMBL:Z68888; NID:g1167859; PID:e219690; PIDN:CAA93116.1

A;Experimental source: clone Sfurin 6; ovary

C;Function:

A;Description: responsible for the endoproteolytic processing of proproteins with specificity for paired basic amino acid residues

C;Keywords: hydrolase; serine proteinase

Query Match 8.2%; Score 79.5; DB 2; Length 1299;
Best Local Similarity 24.1%; Pred. No. 40;
Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

```
Qy          8 CSQNEYFDSLHACIPCQLRCS-----SNTPLTLCQRYCNAS----VTNSVKGTNAIL-W 57
              ||:      | | : |:||      ||          :||||      | :||      : :|| | | |
Db          1150 CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAGKRRIA EW 1205

Qy          58 TCLGLS-----LIISLAV-----FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
              | :              :::||          |: : : : | | | : |
Db          1206 GALHTAPSADAAPSVAVVTIAVCAAAGLFIITVLVVLQAHSPREKKTRKTSVRG----- 1259

Qy          102 IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDS DH 142
              :| ||          ||| ::||      | :      |: :|
Db          1260 --VEYSR-----LPRTDVDFTV----LTSCTDQEGPVEYEH 1289
```

RESULT 10

D64469

potassium channel homolog - Methanococcus jannaschii

C;Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: D64469

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley,

C;Comment: This protein function as inhibitory cell-surface molecule against cell activation.
 C;Genetics:
 A;Map position: 7
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>
 F;24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status predicted <EID>
 F;636-674/Domain: transmembrane #status predicted <TMM>
 F;675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 8.1%; Score 78; DB 2; Length 841;
 Best Local Similarity 22.7%; Pred. No. 35;
 Matches 46; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

```

Qy      9 SQNEYFDSLLHACIPCQLRCS----SNTPLTLCQRYCNASVTNSVKGTNAILWTCLGLSL 64
      :|| | | | | :| | :||| | : : | : | :|:|:
Db      598 AQNSSFYLLSSASAPVELTVSGPIETSTPPPT-----MSMPLGGLHMYLKALIGVSV 649

Qy      65 IISLAVFVLMFLL--RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRG---- 118
      | :|:|:|:| | : : || | | :| | :|
Db      650 AFILFLFILIFILLRRRHRGKFRKDVQKEK-----DLQLSSGAEEPITRKGELQK 699

Qy      119 -----LEYTVEECTCEDCIK----SKPKVDSDDHCFPLPAMEEGATILVTTKTN 162
      | :||: || : : | : | :| |
Db      700 RPNPAAATQEESLYASVEDMQTEDGVELNSWTPPEED-----PQGET----- 741

Qy      163 DYCKSLPAAL-SATEIEKSISAR 184
      | : | : | | : | : |
Db      742 -YQVKPSRLRKAGHVSPSVMR 763
  
```

RESULT 12

D86345

hypothetical protein Fl6F4.10 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C;Accession: D86345

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-738 <STO>
A;Cross-references: GB:AE005172; NID:g8920639; PIDN:AAF81361.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase
PRO25; protein kinase homology

Query Match 8.0%; Score 77.5; DB 2; Length 738;
Best Local Similarity 26.2%; Pred. No. 35;
Matches 28; Conservative 21; Mismatches 45; Indels 13; Gaps 5;

```
Qy      8 CSQNEYFDSLL-HACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCGLGLSLII 66
      || :  :: || | : | || | : | : | : | : |
Db      294 CSGDSTCENKLGHFRCNCRSRYELNTTTNTCKPKGNPEY---VEWTTIVLGTTFIGF-LVI 349

Qy      67 SLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL-----GMANIDLE 105
      || :  :: | : : | : | : | : | : | : |
Db      350 LLAISCIIEHKMKNTKDTELRRQQFFEQNGGGLMLQRLSGAGPSNVDVK 396
```

RESULT 13
T01733

hypothetical protein A_IG002N01.31 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
C;Accession: T01733
R;Scheet, P.; Maggi, L.
submitted to the EMBL Data Library, June 1997
A;Description: The sequence of A. thaliana IG002N01.
A;Reference number: Z14407
A;Accession: T01733
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-968 <SCH>
A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191152
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3;
806/3; 833/3
A;Note: A_IG002N01.31

Query Match 8.0%; Score 77.5; DB 2; Length 968;
Best Local Similarity 21.6%; Pred. No. 45;
Matches 35; Conservative 26; Mismatches 62; Indels 39; Gaps 5;

```
Qy      43 ASVTNSVKG----TNAILWTCGLGLSLIISLAVFVLM-----FLLRKISSEPLK 86
      :|:|:|: |  :: :  ||:|  |:||  || |:: : |
Db      770 SSLTDSISGVFGESSDGVSVVALGVAAAAGLSVFATFEDRKQTLKQVDEFLNTKVAPKELV 829

Qy      87 DEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDS DHCFPL 146
      || | | | |  | : | :  : | :  | |  ||
Db      830 DELKEIGKAL-----LPQSTSNKALPAPATVTAEAESATATTTTVDKP----- 872
```

Qy 147 PAMEEGATILVTTKTND---YCKSLPAALSATEIEKSISAR 184
 : | | : | | | : : | : | : : : | :
 Db 873 --VPEPETVAATTTTVDKVPPEPEPVPEPVPAIEAAVAAQ 912

RESULT 14

T45824

hypothetical protein F2K15.50 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000

C;Accession: T45824

R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.;
 Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.

submitted to the Protein Sequence Database, January 2000

A;Reference number: Z23015

A;Accession: T45824

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-522 <RIE>

A;Cross-references: EMBL:AL132956

A;Experimental source: cultivar Columbia; BAC clone F2K15

C;Genetics:

A;Map position: 3

A;Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3

A;Note: F2K15.50

C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70

Query Match 8.0%; Score 77; DB 2; Length 522;

Best Local Similarity 27.0%; Pred. No. 27;

Matches 27; Conservative 18; Mismatches 37; Indels 18; Gaps 3;

Qy 16 SLLHAC-----IPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTC--LG 61
 ||: || :| | | | : || : : : || :|| ||
 Db 159 SLVLACMRKTSNPDELPSPYQYRSSSRSSLLTTGSRSDSRLWLVK---VIWTAVILG 214

Qy 62 LSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
 |: : |: : | | : |:| :| :| | | : :
 Db 215 LNTVCDALEFIVTTLFVKDTETPIKGDFLSTKSKQLRLVH 254

RESULT 15

F72288

methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: F72288

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
 D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.;
 Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.;
 Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.;
 Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter,
 J.C.; Fraser, C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima.

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72288

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-539 <ARN>
 A;Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36222.1;
 PID:g4981694; TIGR:TM1146
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TM1146
 C;Superfamily: methyl-accepting chemotaxis protein

Query Match 8.0%; Score 77; DB 2; Length 539;
 Best Local Similarity 32.0%; Pred. No. 28;
 Matches 24; Conservative 19; Mismatches 20; Indels 12; Gaps 5;

```

Qy      42 NASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD---EFKNTGSGLLG 98
      | |:| ::| | | :   | :: : |:|: :| | ::| |||   :|   |:|
Db      150 NVSMTKNIK-RNIIF-----LVVCAAAMFIAIFTTRNLTT-PLKKLAVLVENLSHGVL- 202

Qy      99 MANIDLEKSRTGDEI 113
      |::|| |: |||
Db      203 --NVEIEKIRSKDEI 215
  
```

Search completed: April 19, 2004, 13:23:35
 Job time : 12.2222 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:21:03 ; Search time 28.7737 Seconds
 (without alignments)
 1762.857 Million cell updates/sec

Title: PCT-US03-05147-1
 Perfect score: 964
 Sequence: 1 MLQMAGQCSQNEYFDSLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA:*
 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	964	100.0	184	13	US-10-077-438-1	Sequence 1, Appli
2	964	100.0	184	13	US-10-077-438-7	Sequence 7, Appli
3	964	100.0	184	13	US-10-077-137-1	Sequence 1, Appli
4	964	100.0	184	13	US-10-077-137-7	Sequence 7, Appli
5	964	100.0	184	14	US-10-068-725-2	Sequence 2, Appli
6	964	100.0	184	14	US-10-151-882-47	Sequence 47, Appl
7	964	100.0	184	14	US-10-115-192-8	Sequence 8, Appli
8	964	100.0	184	14	US-10-008-063-7	Sequence 7, Appli
9	964	100.0	184	14	US-10-152-363A-27	Sequence 27, Appl
10	964	100.0	184	14	US-10-216-074-11	Sequence 11, Appl
11	964	100.0	184	15	US-10-087-080-39	Sequence 39, Appl
12	950	98.5	181	9	US-09-854-864-5	Sequence 5, Appli
13	950	98.5	181	12	US-09-855-158-5	Sequence 5, Appli
14	572	59.3	185	9	US-09-854-864-11	Sequence 11, Appl
15	572	59.3	185	12	US-09-855-158-11	Sequence 11, Appl
16	572	59.3	185	14	US-10-216-074-17	Sequence 17, Appl
17	323	33.5	58	9	US-09-854-864-21	Sequence 21, Appl
18	323	33.5	58	12	US-09-855-158-21	Sequence 21, Appl
19	311.5	32.3	117	9	US-09-854-864-12	Sequence 12, Appl
20	311.5	32.3	117	12	US-09-855-158-12	Sequence 12, Appl
21	286.5	29.7	302	14	US-10-115-192-12	Sequence 12, Appl
22	286	29.7	283	9	US-09-854-864-9	Sequence 9, Appli
23	286	29.7	283	12	US-09-855-158-9	Sequence 9, Appli
24	284	29.5	51	9	US-09-854-864-6	Sequence 6, Appli
25	284	29.5	51	12	US-09-855-158-6	Sequence 6, Appli
26	264	27.4	207	13	US-10-077-438-3	Sequence 3, Appli
27	264	27.4	207	13	US-10-077-137-3	Sequence 3, Appli
28	201	20.9	34	9	US-09-854-864-7	Sequence 7, Appli
29	201	20.9	34	12	US-09-855-158-7	Sequence 7, Appli
30	201	20.9	81	9	US-09-854-864-13	Sequence 13, Appl
31	201	20.9	81	12	US-09-855-158-13	Sequence 13, Appl
32	187	19.4	281	9	US-09-854-864-10	Sequence 10, Appl
33	187	19.4	281	12	US-09-855-158-10	Sequence 10, Appl
34	158	16.4	42	14	US-10-145-206-197	Sequence 197, App
35	116.5	12.1	175	14	US-10-008-063-13	Sequence 13, Appl
36	104	10.8	21	9	US-09-854-864-8	Sequence 8, Appli
37	104	10.8	21	12	US-09-855-158-8	Sequence 8, Appli
38	100	10.4	185	14	US-10-251-947-2	Sequence 2, Appli
39	93	9.6	184	12	US-10-087-192-984	Sequence 984, App
40	93	9.6	184	14	US-10-008-063-2	Sequence 2, Appli
41	93	9.6	184	14	US-10-152-363A-60	Sequence 60, Appl
42	91	9.4	171	14	US-10-251-947-4	Sequence 4, Appli
43	91	9.4	171	14	US-10-251-947-7	Sequence 7, Appli
44	90.5	9.4	170	14	US-10-251-947-6	Sequence 6, Appli
45	86.5	9.0	392	14	US-10-152-363A-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1

US-10-077-438-1

; Sequence 1, Application US/10077438

; Publication No. US20020165156A1

; GENERAL INFORMATION:

; APPLICANT: MacKay, Fabienne

```

; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

```

```

Query Match          100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MLQMAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
        |||
Db      1 MLQMAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        |||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
        |||
Db    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy     181 ISAR 184
        |||
Db     181 ISAR 184

```

RESULT 2

US-10-077-438-7

```

; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal

```

```
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7
```

```
Query Match          100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy    181 ISAR 184
          ||||
Db    181 ISAR 184
```

RESULT 3

US-10-077-137-1

```
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
```

```
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1
```

```
Query Match          100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          |||
Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
          |||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
          |||
Db    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy    181 ISAR 184
          |||
Db    181 ISAR 184
```

RESULT 4

US-10-077-137-7

```
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
```

```
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7
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```
Query Match          100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy     181 ISAR 184
        ||||
Db     181 ISAR 184
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RESULT 5

US-10-068-725-2

```
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2
```

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLQ MAGQCSQNEYFDSL LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          |||
Db      1 MLQ MAGQCSQNEYFDSL LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
          |||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
          |||
Db    121 YTVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy    181 ISAR 184
          |||
Db    181 ISAR 184
```

RESULT 6

US-10-151-882-47

; Sequence 47, Application US/10151882

; Publication No. US20030059862A1

; GENERAL INFORMATION:

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

; FILE REFERENCE: PF554

; CURRENT APPLICATION NUMBER: US/10/151,882

; CURRENT FILING DATE: 2002-05-22

; PRIOR APPLICATION NUMBER: 60/293,100

; PRIOR FILING DATE: 2001-05-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 47

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-151-882-47

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQ MAGQCSQNEYFDSL LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          |||
Db      1 MLQ MAGQCSQNEYFDSL LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
          |||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy    121 YTVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
          |||
Db    121 YTVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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Qy 181 ISAR 184
||||
Db 181 ISAR 184

RESULT 7

US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
|||||
Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
|||||
Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy 121 YTVEECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
|||||
Db 121 YTVEECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
||||
Db 181 ISAR 184

RESULT 8

US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.

```
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7
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Query Match          100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

QY     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

QY    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

QY    181 ISAR 184
      ||||
Db    181 ISAR 184
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RESULT 9

US-10-152-363A-27

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; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27
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Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

Qy      121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy      181 ISAR 184
        ||||
Db      181 ISAR 184
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RESULT 10

US-10-216-074-11

; Sequence 11, Application US/10216074

; Publication No. US20030148445A1

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/10/216,074

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US/09/565,423

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-216-074-11

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.6e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

Qy      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
```

Qy 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||
 Db 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||
 Qy 181 ISAR 184
 |||
 Db 181 ISAR 184

RESULT 11

US-10-087-080-39
 ; Sequence 39, Application US/10087080
 ; Publication No. US20030235820A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Markowitz, Sanford David
 ; APPLICANT: Eos Biotechnology, Inc.
 ; APPLICANT: Case Western Reserve University
 ; TITLE OF INVENTION: No. US20030235820A1el Methods of Diagnosis of Metastatic
 Colorectal
 ; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
 ; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
 ; FILE REFERENCE: 018501-000840US
 ; CURRENT APPLICATION NUMBER: US/10/087,080
 ; CURRENT FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/272,206
 ; PRIOR FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: US 60/281,149
 ; PRIOR FILING DATE: 2001-04-02
 ; PRIOR APPLICATION NUMBER: US 60/284,555
 ; PRIOR FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 39
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
 ; OTHER INFORMATION: 17 (TNFRSF17)
 US-10-087-080-39

Query Match 100.0%; Score 964; DB 15; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.6e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQ MAGQCSQNEYFDSL LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
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 Db 1 MLQ MAGQCSQNEYFDSL LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 |||
 Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 |||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 |||
 Qy 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||

Db 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
||||
Db 181 ISAR 184

RESULT 12

US-09-854-864-5

; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 98.5%; Score 950; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEYFDSLHLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCGLGLS 63
|||||
Db 1 MAGQCSQNEYFDSLHLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCGLGLS 60

Qy 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEEYTV 123
|||||
Db 61 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEEYTV 120

Qy 124 EECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
|||||
Db 121 EECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180

Qy 184 R 184
|
Db 181 R 181

RESULT 13

US-09-855-158-5

; Sequence 5, Application US/09855158
; Publication No. US20020086018A1

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; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA, BLYS/AGP-
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5
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Query Match          98.5%; Score 950; DB 12; Length 181;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      4 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 60

Qy     64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLETV 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLETV 120

Qy    124 EECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180

Qy    184 R 184
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Db    181 R 181
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RESULT 14
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
```

; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-854-864-11

Query Match 59.3%; Score 572; DB 9; Length 185;
 Best Local Similarity 62.6%; Pred. No. 2.3e-52;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTNAILWTCGLS 63
 || || :||||| || ||||: || ||| ||: |||:|||| :|| |||:
 Db 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
 Qy 64 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
 |:|:|:| : |||||: | |||| :| | | | :| :| | | |
 Db 59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSQAQLDKADTELTRIRAGDDRI FPRSL 118
 Qy 120 EYTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 |||||:|||| ||| ||||| ||||| || | |:| || | :
 Db 119 EYTVEECTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTGDYKGSSVPTALQSVGMGM 178
 Qy 178 EKSISAR 184
 || |
 Db 179 EKPTHTR 185

RESULT 15

US-09-855-158-11
 ; Sequence 11, Application US/09855158
 ; Publication No. US20020086018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
 BCMA, BLYS/AGP-
 ; TITLE OF INVENTION: 3, AND TACI
 ; FILE REFERENCE: A-686A
 ; CURRENT APPLICATION NUMBER: US/09/855,158
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-855-158-11

Query Match 59.3%; Score 572; DB 12; Length 185;

Best Local Similarity 62.6%; Pred. No. 2.3e-52;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

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Qy      4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCGLGS 63
      || || :||||| || ||||: || ||| ||: ||:|||| :|| ||:
Db      1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58

Qy      64 LIISLAVFVLMFLLRKISSEPLKDEFKN---TGSGLLGMANIDLEKSRTGDEIILPRGL 119
      |:|:|:| : | |:|:|: | ||| :| | | | :| :| : | |:| || |
Db      59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSALDKADTELTRIRAGDDRIFPRSL 118

Qy      120 EYTVEECTCEDCIKSKPKVDSDFHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
      |||||:|||| ||| ||||| ||||| || | |:| || | :
Db      119 EYTVEECTCEDCVKSKPKGDSDFHCFPLPAMEEGATILVTTKTGDYKSSVPTALQSVGMGM 178

Qy      178 EKSISAR 184
      || |
Db      179 EKPTHTR 185
  
```

Search completed: April 19, 2004, 13:25:47
 Job time : 28.7737 secs

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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:32 ; Search time 27.2593 Seconds
(without alignments)
2129.748 Million cell updates/sec

Title: PCT-US03-05147-1
Perfect score: 964
Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	116.5	12.1	175	11	Q8R4W8	Q8r4w8 mus musculu
2	92.5	9.6	334	2	Q8GM90	Q8gm90 symbiont ba
3	88.5	9.2	217	16	Q97D61	Q97d61 clostridium
4	86.5	9.0	804	11	Q80XB3	Q80xb3 mus musculu
5	86.5	9.0	809	11	Q80XB2	Q80xb2 mus musculu
6	86.5	9.0	823	11	Q80XB6	Q80xb6 mus musculu
7	86.5	9.0	827	11	Q8CDK8	Q8cdk8 mus musculu
8	86.5	9.0	834	11	Q8BH12	Q8bh12 mus musculu
9	86.5	9.0	842	11	Q8R056	Q8r056 mus musculu
10	85.5	8.9	1193	5	Q9Y1X8	Q9y1x8 ephydatia f
11	83.5	8.7	938	10	Q8RWV7	Q8rww7 arabidopsis
12	83.5	8.7	1998	10	Q9STR8	Q9str8 arabidopsis
13	83	8.6	449	11	Q8C6R5	Q8c6r5 mus musculu
14	83	8.6	474	11	Q8C9L4	Q8c9l4 mus musculu
15	82	8.5	327	6	O97491	O97491 ovis aries
16	82	8.5	967	11	Q8C2G0	Q8c2g0 mus musculu
17	81.5	8.5	314	11	Q8VEV6	Q8vev6 mus musculu
18	81.5	8.5	2233	5	Q94711	Q94711 paramecium
19	81	8.4	595	10	Q39191	Q39191 arabidopsis
20	81	8.4	773	5	O01892	O01892 caenorhabdi
21	80.5	8.4	314	11	Q7TQQ9	Q7tqq9 mus musculu
22	80.5	8.4	487	5	Q8IN99	Q8in99 drosophila
23	80	8.3	735	10	O81820	O81820 arabidopsis
24	79.5	8.2	153	2	Q8KLY1	Q8kly1 pseudomonas
25	79.5	8.2	1299	5	Q26489	Q26489 spodoptera
26	79	8.2	1200	13	Q802S1	Q802s1 fugu rubrip
27	78.5	8.1	314	11	Q8VFW0	Q8vfw0 mus musculu
28	78.5	8.1	485	4	Q9H677	Q9h677 homo sapien
29	78.5	8.1	522	4	Q8N6T0	Q8n6t0 homo sapien
30	78.5	8.1	789	10	Q8LQ43	Q8lq43 oryza sativ
31	78	8.1	841	11	Q8R2Z1	Q8r2z1 mus musculu
32	77.5	8.0	738	10	Q9LMN6	Q9lmn6 arabidopsis
33	77.5	8.0	738	10	O81819	O81819 arabidopsis
34	77.5	8.0	853	15	Q9YKU7	Q9yku7 human immun
35	77.5	8.0	968	10	O04623	O04623 arabidopsis
36	77	8.0	522	10	Q9M3B3	Q9m3b3 arabidopsis
37	77	8.0	539	16	Q9X0N0	Q9x0n0 thermotoga
38	76.5	7.9	357	5	Q9XV87	Q9xv87 caenorhabdi
39	76.5	7.9	656	10	Q9FJE3	Q9fje3 arabidopsis
40	76.5	7.9	1404	5	O45251	O45251 caenorhabdi
41	76	7.9	797	3	Q872A6	Q872a6 neurospora
42	76	7.9	1805	11	Q63661	Q63661 rattus norv
43	75.5	7.8	202	16	Q8D6L4	Q8d6l4 vibrio vuln
44	75.5	7.8	567	12	Q8JKV7	Q8jkv7 heliothis z
45	75	7.8	450	16	Q97E85	Q97e85 clostridium

ALIGNMENTS

RESULT 1

Q8R4W8

ID Q8R4W8 PRELIMINARY; PRT; 175 AA.
AC Q8R4W8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DR Pfam; PF00698; Acyl_transf; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 334 AA; 38018 MW; 6C42D1FFEC5E35F3 CRC64;

Query Match 9.6%; Score 92.5; DB 2; Length 334;
Best Local Similarity 25.0%; Pred. No. 0.33;
Matches 42; Conservative 22; Mismatches 65; Indels 39; Gaps 7;

QY 14 FDSLLHACIPCQLRCSSNTPPLTCQRYCNAS--VTNSVKGTNAILWTCLGLSLIISLA-- 69
|| |:| | | :| | : : : || : |||
Db 72 FDRLIH-----THPALFMVQYALAKSLLARGLPAPDFLIGASLGEFIAISLAGD 120

QY 70 VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCE 129
| | | | | ||:| |: || : || : :
Db 121 THVENILFNLIKQARLFDEYCNAGAMLLVIDHID-----TFSTTPAFSK 164

QY 130 DCIKSKPKVDSHCFPLPAMEEGATILVT---TKTNDYCKSLPAALS 173
|| : : ||| : | || | || | |: || : :
Db 165 DC--ELAGINFDFHCFVVSGRPFG---ILQTRKSLTKQNIACQLLPVSIA 208

RESULT 3

Q97D61

ID Q97D61 PRELIMINARY; PRT; 217 AA.
AC Q97D61;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amino acid ABC transporter, permease component.
GN CAC3619.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007858; AAK81542.1; -.
DR PIR; C97344; C97344.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
KW Complete proteome.
SQ SEQUENCE 217 AA; 23743 MW; 36738BCDCODE8A2F CRC64;

Query Match 9.2%; Score 88.5; DB 16; Length 217;

Best Local Similarity 24.8%; Pred. No. 0.52;
Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

```
Qy      16 SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL 62
      | | : | | | : | | | : | | | | | | | | | | | |
Db      4 SSLNKVIPVLLDGTTRITLLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT 63

Qy      63 SLIISLAVFV--LMFLLRKISSEPLKDEF---KNTGS-----GLLGMANIDLEKSR 108
      | : | | : | | | : | : | : | : | : | : | : |
Db      64 PLLLQLYVYYYGLPFLSDKLTMTMPKAAAILGLSLNSGAYIAEIIIRGGILAIIDNGQFEASK 123

Qy     109 -----TGDEIILPRGLEYTVEEC-----TCEDCI-KSKPKVDS DH 142
      | | | | : : : | | | : : | : | : | : |
Db     124 ALGLTYGQTMKRIILPQAIRVVIIPPCGNEFIAMIKDTSLSVSVITMEELLRKAQLLVSSSG 183

Qy     143 CFPLPAMEEGA--TILVTTKTNDYCKSLPAALSATEIEKSIS 182
      | : | | | | : | | | : |
Db     184 DAVTPYLFAGIFYLILTTIFTGIFSK-----IEKKLS 215
```

RESULT 4

Q80XB3

ID Q80XB3 PRELIMINARY; PRT; 804 AA.
AC Q80XB3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prominin-1 T2 isoform.
GN PROM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Fargeas C.A., Huttner W.B., Corbeil D.;
RT "Identification and characterization of a mouse prominin-1 splice
RT variant.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY223521; AA072429.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 804 AA; 89983 MW; CFC9D6E8BCF9FF16 CRC64;

Query Match 9.0%; Score 86.5; DB 11; Length 804;
Best Local Similarity 22.7%; Pred. No. 3.9;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

```
Qy      18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
      | | | | | : | : | | | | : | : |
Db     112 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNA PCRRKCLGLSLLVICLLMSLGIIY 162

Qy      78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
```

```

      : : : | | | | : : | : : | : : |
Db      163 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNTKNKA 213

Qy      130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
      | | | | | | | : | : | : | : : |
Db      214 FSDLGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 266

Qy      173 ---SATEIEKSISA 183
      : | : : : : :
Db      267 LQDAATQLNTNLSS 280

```

RESULT 5

Q80XB2

```

ID      Q80XB2          PRELIMINARY;          PRT;      809 AA.
AC      Q80XB2;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Prominin-1 T3 isoform.
GN      PROM1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c; TISSUE=Testis;
RA      Fargeas C.A., Huttner W.B., Corbeil D.;
RT      "Identification and characterization of a mouse prominin-1 splice
RT      variant.";
RL      Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY223522; AA072430.1; -.
DR      GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR      GO; GO:0005488; F:binding; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ      SEQUENCE      809 AA; 90605 MW; BC991E100C623AE1 CRC64;

```

```

Query Match          9.0%; Score 86.5; DB 11; Length 809;
Best Local Similarity 22.7%; Pred. No. 3.9;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

```

```

Qy      18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
      | | | | | | | : | : | | | | : : | :
Db      117 LVGCFFCMCRC-----CNK-CGGEMHQKQKQONAPCRRKCLGLSLLVICLLMSLGIIY 167

Qy      78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
      : : : : | | | | | | | : : | : : | : : |
Db      168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNTKNKA 218

Qy      130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
      | | | | | | | : | : | : | : : |
Db      219 FSDLGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271

Qy      173 ---SATEIEKSISA 183

```

Db 272 LQDAATQLNTNLSS 285

RESULT 6

Q80XB6

ID Q80XB6 PRELIMINARY; PRT; 823 AA.
AC Q80XB6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prominin T4 isoform.
GN PROM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Fargeas C.A., Huttner W.B., Corbeil D.;
RT "Identification and characterization of a novel mouse prominin isoform
RT with an alternative C-terminal domain."
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY099088; AAM28245.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 823 AA; 92225 MW; 9EF01A18DB84EFAC CRC64;

Query Match 9.0%; Score 86.5; DB 11; Length 823;
Best Local Similarity 22.7%; Pred. No. 4;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVIMFLL 77
| | | | | : | : | | | | : | :
Db 117 LVGCFFCMCRC-----CNK-CGGMHQKQKQNA PCRRKCLGLSLLVICLMSLGIY 167

QY 78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
:::: : | | | | | : : | : : | | : |
Db 168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLETTPKQIDYVVEQYTNTKNKA 218

QY 130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
| | | | | : | : | | | : : : |
Db 219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271

QY 173 ---SATEIEKSISA 183
: | | : : : | :
Db 272 LQDAATQLNTNLSS 285

RESULT 7

Q8CDK8

ID Q8CDK8 PRELIMINARY; PRT; 827 AA.
AC Q8CDK8;


```

DE Prominin T1 isoform.
GN PROM1 OR 4932416E19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RA Fargeas C.A., Huttner W.B., Corbeil D.;
RT "Identification and characterization of a mouse prominin isoform.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF305215; AAO11840.1; -.
DR EMBL; AK030027; BAC26745.1; -.
DR MGD; MGI:1100886; Prom1.
DR GO; GO:0005903; C:brush border; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005902; C:microvillus; IDA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR008795; Prominin.
DR Pfam; PF05478; Prominin; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 834 AA; 93444 MW; 5ABA26C80F636E45 CRC64;

```

Qy	18	LHACIPQCQLRCSNSTPPLTCQRYCNASVTNSVKGTNAILWTCGLGLSLIISLAVFVLMFLL	77
		: : : : :	
Db	117	LVGCFFCMCRC-----CNK-CGGEMHQKQKQAPCRRKCLGLSLLVICLLMSLGIYY	167
Qy	78	RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE----	129
		: : : : : : : : : : :	
Db	168	GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNNTKNKA	218
Qy	130	----DCIKS-----KPKVDSHDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL--	172
		: : : : :	
Db	219	FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS	271
Qy	173	---SATEIEKSISA	183
		: : : : :	
Db	272	LQDAATQNLNTNLSS	285


```

Qy      57 WTCLGLSLIISLA---VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEI 113
      |  ::| ||   | :| : |:  : |: ::|   : :|   |::|
Db      772 GIVFGSIVVIFLATSIVLILFIVYRRYEHKVFKNRTQSTA---MCYSN-----GNET 820

Qy      114 ILPRGLEYTVEECTCEDCIKSKPKVDS DH----CFPLPAMEEGATI 155
      : |               ||: |   | |:|:| :
Db      821 LRP-----PKLPPDATRLIITPETALEOGQVL 847

```

RESULT 11

Q8RWV7

```

ID      Q8RWV7          PRELIMINARY;          PRT;    938 AA.
AC      Q8RWV7;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
GN      AT3G48195.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA      Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA      Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA      Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA      Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA      Meyers M.C., Miranda M., Narusaka M., Nguyen C., Palm C.J.,
RA      Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA      Davis R.W., Ecker J.R., Theologis A.;
RT      "Arabidopsis Full Length cDNA Clones.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY091078; AAM13898.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005489; F:electron transporter activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR000515; BPD_transp.
DR      InterPro; IPR000345; CytC_heme_BS.
DR      InterPro; IPR001683; PX.
DR      Pfam; PF00787; PX; 1.
DR      SMART; SM00312; PX; 1.
DR      PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
DR      PROSITE; PS00190; CYTOCHROME_C; 2.
DR      PROSITE; PS50195; PX; 1.
KW      Hypothetical protein.
SQ      SEQUENCE      938 AA;  103602 MW;  3E78395D65D75C95 CRC64;

```

Query Match 8.7%; Score 83.5; DB 10; Length 938;
Best Local Similarity 29.4%; Pred. No. 9.6;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Qy 38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS 94
 :|||:| || || :: | | :| ||:| |
 Db 29 ERYCSA---NSALGTPSM---C-----SSTGPFQDSEFENFSLGP 62

Qy 95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDS DHCFPLPAM 149
 |: ::::|: || || ||: : | :| | | | |
 Db 63 SLVKLSSLDM--SRLGD-----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M 113

Qy 150 EEGATI 155
 : ||||
 Db 114 DGGATI 119

RESULT 12

Q9STR8

ID Q9STR8 PRELIMINARY; PRT; 1998 AA.
 AC Q9STR8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN T24C20_80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL096856; CAB51067.1; -.
 DR PIR; T13009; T13009.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000515; BPD_transp.
 DR InterPro; IPR001683; PX.
 DR Pfam; PF00787; PX; 1.
 DR SMART; SM00312; PX; 1.
 DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
 DR PROSITE; PS50195; PX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1998 AA; 223513 MW; 8B3D6A03CD248F55 CRC64;

Query Match 8.7%; Score 83.5; DB 10; Length 1998;
 Best Local Similarity 29.4%; Pred. No. 23;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Qy 38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS 94

```

      :|||:|  ||  || ::  |  | :| | :| ||:|  |
Db      1089 ERYCSA---NSALGTPSM---C-----SSTGPFQDSEFENFSLGP 1122

Qy      95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDFCFPLPAM 149
      | : ::::|: || ||  ||: : | :|  | |  | :| | | |
Db      1123 SLVKLSSLDM--SRLGD-----RGIHFFDEGGSCNGRSSAPGLNTGNVNIDMCGDL--M 1173

Qy      150 EEGATI 155
      : ||||
Db      1174 DGGATI 1179

```

RESULT 13

Q8C6R5

```

ID      Q8C6R5          PRELIMINARY;          PRT;      449 AA.
AC      Q8C6R5;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Protein tyrosine kinase 2 beta (Fragment).
GN      PTK2B.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Oviduct;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
DR      EMBL; AK054002; BAC35615.1; -.
DR      MGD; MGI:104908; Ptk2b.
DR      GO; GO:0005515; F:protein binding; IPI.
DR      GO; GO:0004672; F:protein kinase activity; IDA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR      InterPro; IPR000299; Band_4.1.
DR      SMART; SM00295; B41; 1.
DR      PROSITE; PS50057; FERM_3; 1.
FT      NON_TER      449      449
SQ      SEQUENCE      449 AA; 51577 MW; D3565BCBA7D32B84 CRC64;

```

```

Query Match      8.6%; Score 83; DB 11; Length 449;
Best Local Similarity 26.9%; Pred. No. 4.6;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

```

```

Qy      88 EFKNTGSGLLGMANIDLEKS-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
      :| ||  | | |||| | |  | | :| ||:|  : |  | : :
Db      249 KFFNT---LAGFANIDQETRYCELIQGWNIITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305

Qy      139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
      | | ||  :  |||  :: ||:  ||:
Db      306 KSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353

```

RESULT 14

Q8C9L4

ID Q8C9L4 PRELIMINARY; PRT; 474 AA.
AC Q8C9L4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein tyrosine kinase 2 beta.
GN PTK2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK041878; BAC31090.1; -.
DR MGD; MGI:104908; Ptk2b.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; IDA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000299; Band_4.1.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS50057; FERM 3; 1.
SQ SEQUENCE 474 AA; 54201 MW; A1A83BCB191B55FB CRC64;

Query Match 8.6%; Score 83; DB 11; Length 474;

Best Local Similarity 26.9%; Pred. No. 4.9;

Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

Qy 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYYTVEECTCEDCIKSKPKV 138
:| || | | ||| | | | | :| |:| : | | : :
Db 249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCIAEFKQI 305
Qy 139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
| | || : ||| :: ||: ||:
Db 306 KSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353

RESULT 15

O97491

ID O97491 PRELIMINARY; PRT; 327 AA.
AC O97491;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas protein.
GN FAS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
 RT "Cloning of sheep fas antigen."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB011671; BAA37093.1; -.
 DR HSSP; P25445; 1DDF.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR008063; Fas_receptor.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR PRINTS; PR01680; FASRECEPTOR.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;

Query Match 8.5%; Score 82; DB 6; Length 327;
 Best Local Similarity 23.0%; Pred. No. 4;
 Matches 54; Conservative 25; Mismatches 68; Indels 88; Gaps 15;

Qy 8 CSQ-NEYFDSLHA--CIPCQL-----RCSSN-----T 32
 ||: ||| | |: || |: || ||
 Db 84 CSEGNEYTDKSHHSDKCIRCSVCDEEHGLEVEHNCTRTQNTKCRCKSNFFCNSSPCEHCN 143

 Qy 33 PPLTCQ----RYCNASVTNSVKG----TNAILWTCLGLSLIISLAVFVLMFLLRK----- 79
 | ||: | : || ||: || | | |: | : : : : |:
 Db 144 PCTTCEHGIIEKCTPTSNTKCKGSRSHNTS-LWALLILLILLILIFLIYKVVRRRRRRNKK 202

 Qy 80 ---ISSEPLKDEFKNTGSGLLGMANIDLEKSRTG-----DEIILPRGLEYYTVEEC 126
 | ||: | : ||: ||: || | | : | : |:
 Db 203 NGNCVSAASSDEGRQ-----LNLTDVDLGKYIPSI AELMKITEVKEFVRKNGM----EEA 253

 Qy 127 TCEDCIKSKPKVDS DHCFFLPAMEEGATIL-----VTTKTNDYC---KSLPAALS 173
 :| : |: | |: :| | || |: || |:
 Db 254 KIDDIMH-----DNLH-----ETAEQKVQLLRKQYQSHGKKNAYCTLTKNLPKALA 299

Search completed: April 19, 2004, 13:22:55
 Job time : 29.2593 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:02 ; Search time 7.57202 Seconds
(without alignments)
1265.305 Million cell updates/sec

Title: PCT-US03-05147-1
Perfect score: 964
Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	964	100.0	184	1	TR17_HUMAN	Q02223 homo sapien
2	572	59.3	185	1	TR17_MOUSE	O88472 mus musculu
3	116.5	12.1	175	1	T13C_MOUSE	Q9d8d0 mus musculu
4	94	9.8	323	1	TNR6_BOVIN	P51867 bos taurus
5	93	9.6	184	1	T13C_HUMAN	Q96rj3 homo sapien
6	86.5	9.0	867	1	PML1_MOUSE	O54990 mus musculu
7	82	8.5	1009	1	FAK2_MOUSE	Q9qvp9 m protein t
8	82	8.5	1009	1	FAK2_RAT	P70600 rattus norv
9	79.5	8.2	1009	1	FAK2_HUMAN	Q14289 h protein t
10	78.5	8.1	293	1	T13X_HUMAN	O14836 homo sapien
11	78.5	8.1	343	1	MJK2_METJA	Q58752 methanococc
12	77	8.0	249	1	T13X_MOUSE	Q9et35 mus musculu
13	76	7.9	748	1	CI84_NEUCR	O42637 neurospora
14	75.5	7.8	638	1	YCSB_SCHPO	O74910 schizosacch
15	75	7.8	849	1	SRK6_BRAOL	Q09092 brassica ol
16	74.5	7.7	384	1	ERD1_KLULA	P41771 kluyveromyc
17	72.5	7.5	1013	1	PRML_DROME	P82295 drosophila

18	71.5	7.4	105	1	Y078_NPVOP	O10331	orgyia pseu
19	71.5	7.4	330	1	OR08_MOUSE	Q8vfl3	mus musculu
20	71.5	7.4	627	1	Y017_RICPR	Q9zec6	rickettsia
21	71	7.4	227	1	COMB_THEMEA	Q9wzq4	thermotoga
22	71	7.4	314	1	OR11_MOUSE	Q8vgr9	mus musculu
23	70.5	7.3	154	1	CYY1_HUMAN	Q96j86	homo sapien
24	70.5	7.3	188	1	Y101_UREPA	Q9pr43	ureaplasma
25	70.5	7.3	1203	1	MGR5_RAT	P31424	rattus norv
26	70.5	7.3	1877	1	PCK5_MOUSE	Q04592	mus musculu
27	70.5	7.3	2715	1	G156_PARPR	P13837	paramecium
28	70	7.3	654	1	HS70_TRIRU	O93866	trichophyto
29	69.5	7.2	573	1	TLPC_BACSU	P39209	bacillus su
30	69.5	7.2	1212	1	MGR5_HUMAN	P41594	homo sapien
31	69.5	7.2	5376	1	ZAN_MOUSE	O88799	mus musculu
32	69	7.2	324	1	GC1_MOUSE	P01868	mus musculu
33	69	7.2	352	1	C5AR_RAT	P97520	rattus norv
34	69	7.2	379	1	PANE_YEAST	P38787	saccharomyc
35	69	7.2	393	1	GC1M_MOUSE	P01869	mus musculu
36	69	7.2	416	1	R23B_MOUSE	P54728	mus musculu
37	69	7.2	704	1	MID2_SCHPO	Q9p7y8	schizosacch
38	69	7.2	791	1	SYFB_XANCP	Q8p7z6	xanthomonas
39	69	7.2	943	1	UVRA_STRMU	P72481	streptococc
40	68.5	7.1	213	1	RL1_METMA	Q8py52	methanosarc
41	68.5	7.1	321	1	O5V1_HUMAN	Q9ugf6	homo sapien
42	68.5	7.1	328	1	Y679_CHLMU	Q9pjz7	chlamydia m
43	68.5	7.1	409	1	R23B_HUMAN	P54727	homo sapien
44	68.5	7.1	575	1	CH62_CUCMA	Q05046	cucurbita m
45	68.5	7.1	576	1	CH62_MAIZE	Q43298	zea mays (m

ALIGNMENTS

RESULT 1

TR17_HUMAN

ID TR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein).
GN TNFRSF17 OR BCMA OR BCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Lymph node, and Peripheral blood leukocytes;
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
RA Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
RT by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RL EMBO J. 11:3897-3904(1992).
RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94218235; PubMed=8165126;
 RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
 RT "The BCMA gene, preferentially expressed during B lymphoid
 RT maturation, is bidirectionally transcribed.";
 RL Nucleic Acids Res. 22:1147-1154(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99425270; PubMed=10493829;
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
 RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
 RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
 RT "Genome duplications and other features in 12 Mb of DNA sequence from
 RT human chromosome 16p and 16q.";
 RL Genomics 60:295-308(1999).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT THR-153.
 RX MEDLINE=21419161; PubMed=11528522;
 RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
 RT "Presence of four major haplotypes in human BCMA gene: lack of
 RT association with systemic lupus erythematosus and rheumatoid
 RT arthritis.";
 RL Genes Immun. 2:276-279(2001).
 RN [5]
 RP FUNCTION, AND INTERACTION WITH TRAF1 AND TRAF3.
 RX MEDLINE=20363816; PubMed=10903733;
 RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
 RA Inoue J.-I., Devergne O., Tsapis A.;
 RT "TNF receptor family member BCMA (B cell maturation) associates with
 RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
 RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38
 RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.;
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;

RT "B cell maturation protein is a receptor for the tumor necrosis factor
RT family member TALL-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
CC -!- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
CC humoral immunity. Activates NF-kappa-B and JNK.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
CC and perinuclear Golgi-like structures.
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
CC cells or monocytes.
CC -!- DISEASE: A form of T-cell acute lymphoblastic leukemia (T-ALL) is
CC characterized by a chromosomal translocation t(4;16)(q26;p13)
CC which involves BCMA and IL2.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
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CC -----
DR EMBL; Z14954; CAA78679.1; -.
DR EMBL; Z29575; CAA82691.1; -.
DR EMBL; Z29574; CAA82690.1; -.
DR EMBL; U95742; AAB67251.1; -.
DR EMBL; AB052772; BAB60895.1; -.
DR PIR; S43486; S43486.
DR Genew; HGNC:11913; TNFRSF17.
DR MIM; 109545; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
KW Transmembrane; Chromosomal translocation; Polymorphism.
FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 55 77 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 78 184 CYTOPLASMIC (POTENTIAL).
FT REPEAT 7 41 TNFR-CYS.
FT SITE 3 4 BREAKPOINT FOR TRANSLOCATION TO FORM
FT INTERLEUKIN 2/BCM ONCOGENE.
FT DISULFID 8 21 BY SIMILARITY.
FT DISULFID 24 37 BY SIMILARITY.
FT DISULFID 28 41 BY SIMILARITY.
FT VARIANT 153 153 A -> T.
FT /FTid=VAR_012234.
SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.8e-83;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

QY 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

QY 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 YTVEECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

QY 181 ISAR 184
 ||||
 Db 181 ISAR 184

RESULT 2

TR17_MOUSE

ID TR17_MOUSE STANDARD; PRT; 185 AA.
 AC 088472;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily."
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).

CC -!- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O88472-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O88472-2; Sequence=VSP_006507;
 CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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 CC -----

DR EMBL; AF061505; AAC23799.1; -.

DR EMBL; AK020247; BAB32038.1; -.

DR MGD; MGI:1343050; Tnfrsf17.

KW Receptor; Immune response; Signal-anchor; Transmembrane;

KW Alternative splicing.

FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 70 SIGNAL-ANCHOR
 FT (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
 FT DOMAIN 71 185 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 4 36 TNFR-CYS.
 FT DISULFID 5 18 BY SIMILARITY.
 FT DISULFID 21 32 BY SIMILARITY.
 FT DISULFID 25 36 BY SIMILARITY.
 FT VARSPLIC 87 91 Missing (in isoform 2).
 FT /FTId=VSP_006507.

SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 59.3%; Score 572; DB 1; Length 185;

Best Local Similarity 62.6%; Pred. No. 2.5e-46;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSQNEYFDSLHACIPCQLRCSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63

|| || :||||||| || |||: || ||| ||: |||:||||| :|| |||:

Db 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58

QY 64 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
 |::|||:| : |||||:: | |||| :| | | :| : | ||: | || |
 Db 59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDDRIFPRSL 118

QY 120 EYTVEECTCEDCIKSKPKVSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 |||||:|||| | |||| | ||||| || | |::| || | :
 Db 119 EYTVEECTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTGDYKGSSVPTALQSVMMGM 178

QY 178 EKSISAR 184
 || |
 Db 179 EKPTHTR 185

RESULT 3

T13C_MOUSE

ID T13C_MOUSE STANDARD; PRT; 175 AA.
 AC Q9D8D0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-
 DE activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
 DE 3) (B-cell maturation defect).
 GN TNFRSF13C OR BAFFR OR BCMD OR BR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
 RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RT "BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF.";
 RL Science 293:2108-2111(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
 RC STRAIN=A/J;
 RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
 RA Cancro M.P., Grewal I.S., Dixit V.M.;
 RT "Identification of a novel receptor for B lymphocyte stimulator that
 RT is mutated in a mouse strain with severe B cell deficiency.";
 RL Curr. Biol. 11:1547-1552(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).

RN [4]

RP FUNCTION.

RX MEDLINE=21614654; PubMed=11747827;

RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
 RA Hilbert D.M., Hayes C.E., Cancro M.P.;

RT "Competition for BlyS-mediated signaling through Bcmd/BR3 regulates
 RT peripheral B lymphocyte numbers.";

RL Curr. Biol. 11:1986-1989(2001).

CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BlyS.
 CC Promotes the survival of mature B-cells and the B-cell response.

CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9D8D0-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9D8D0-2; Sequence=VSP_006506;

CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
 CC detected at lower levels in lung and thymus.

CC -!- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
 CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
 CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA
 CC is not detectable. B-cell lymphopoiesis is normal, but the life
 CC span of peripheral B-cells is much reduced.

CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

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 CC -----

DR EMBL; AF373847; AAK91827.1; -.

DR EMBL; AK008142; BAB25490.1; -.

DR MGD; MGI:1919299; Tnfrsf13c.

KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 KW Alternative splicing.

FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 72 92 SIGNAL-ANCHOR

FT (TYPE III MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 38 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 133 143 Missing (in isoform 2).
 FT /FTId=VSP_006506.
 SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 12.1%; Score 116.5; DB 1; Length 175;
 Best Local Similarity 29.4%; Pred. No. 0.00074;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

Qy 7 QCSQNEYFDSLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
 ||:| ||| |: |: |:| || | | :: | | |:|
 Db 21 QCNQTECFDPLVRNCVSCELFHTPDGTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80

 Qy 57 WTCIGLSLI---ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRITGD 111
 | |:|: :|| : || | || :: | : |: : ||
 Db 81 GLILALTIVGLVSLVSWRWRQQRLRTASPDTSSEGVQQE-----SLENVFPVSSET-- 129

 Qy 112 EIILPRGLEYTVEECTCEDCIKSKPKVSDSDHCFPLPAMEEGATILVTTKT 161
 | | | || : |: | |:| | |:| |||||
 Db 130 ----PHASAPTWPLK-EDADSALPR---HSVPVPATELGSTELVTTKT 170

RESULT 4

TNR6_BOVIN

ID TNR6_BOVIN STANDARD; PRT; 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96226401; PubMed=8634151;
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.";
 RL DNA Cell Biol. 15:227-234(1996).
 CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both (By similarity).
 CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC -----
DR EMBL; U34794; AAC48546.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 6.
FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 188 POTENTIAL.
FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
FT REPEAT 45 80 TNFR-CYS 1.
FT REPEAT 81 124 TNFR-CYS 2.
FT REPEAT 125 163 TNFR-CYS 3.
FT DOMAIN 238 306 DEATH.
FT DISULFID 45 56 BY SIMILARITY.
FT DISULFID 57 70 BY SIMILARITY.
FT DISULFID 60 79 BY SIMILARITY.
FT DISULFID 82 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 140 BY SIMILARITY.
FT DISULFID 143 154 BY SIMILARITY.
FT DISULFID 146 162 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;

Query Match 9.8%; Score 94; DB 1; Length 323;
Best Local Similarity 22.1%; Pred. No. 0.18;
Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;

Qy 8 CSQ-NEYFDSLHA--CIPCQL-----RCSSN-----T 32
||: ||| | : || | : || ||


```

Db      82 CSEGNEYTDKSHHSDKCIRCSICDEEHGLEVEQNCTRTRNTKCRCKSNFFCNSSPCEHCN 141
Qy      33 PPLTCQ----RYCNASVTNSVKGTNA---ILWTCLGLSLIISLAVFVLMFLLRKISSEPL 85
      | ||:      | :      ||: :      ||      ||: : : : : : : |
Db      142 PCTTCEHGIIKCTPTSNTKCKGSRSHANSIWAL----LILLIPIVLIIYKVVKSRERNK 197
Qy      86 KDEFKNTGSG-----LLGMANIDL-----EKSRTGD--EILPRGLEYTVEECTCED 130
      |::: |: :      | : :||      |: | : | : | :      || :|
Db      198 KNDYCNSAASNDEGRQLNLTDVDLGKYIPSLAEQMRITEVKEFVRKNGM----EEAKIDD 253
Qy      131 CIKSKPKVDSDFCFPLPAMEEGATILVT-----TKTNDYC---KSLPAALS 173
      :      |: |      |: :|      || ||      |||| ||:
Db      254 IMH-----DNVH----ETAEQKVQLLRNWKYQSHGKKNAYCTLTKSLPKALA 295

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RESULT 5

T13C_HUMAN

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ID      T13C_HUMAN      STANDARD;      PRT;      184 AA.
AC      Q96RJ3;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 13C (B cell-
DE      activating factor receptor) (BAFF receptor) (BAFF-R) (BlyS receptor
DE      3).
GN      TNFRSF13C OR BAFFR OR BR3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC      TISSUE=B-cell lymphoma;
RX      MEDLINE=21442025; PubMed=11509692;
RA      Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA      Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA      Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA      Ambrose C.;
RT      "BAFF-R, a newly identified TNF receptor that specifically interacts
RT      with BAFF.";
RL      Science 293:2108-2111(2001).
RN      [2]
RP      FUNCTION.
RX      MEDLINE=21475520; PubMed=11591325;
RA      Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA      Cancro M.P., Grewal I.S., Dixit V.M.;
RT      "Identification of a novel receptor for B lymphocyte stimulator that
RT      is mutated in a mouse strain with severe B cell deficiency.";
RL      Curr. Biol. 11:1547-1552(2001).
CC      -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BlyS.
CC      Promotes the survival of mature B-cells and the B-cell response.
CC      -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q96RJ3-1; Sequence=Displayed;
CC      Name=2;

```

CC IsoId=Q96RJ3-2; Sequence=VSP_006505;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
 CC in resting B-cells. Detected at lower levels in activated B-cells,
 CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
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 CC -----
 DR EMBL; AF373846; AAK91826.1; -.
 DR PDB; 1MPV; 30-OCT-02.
 DR Genew; HGNC:17755; TNFRSF13C.
 DR MIM; 606269; -.
 DR InterPro; IPR001368; TNFR_c6.
 DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
 DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing; 3D-structure.
 FT DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 79 99 SIGNAL-ANCHOR
 FT (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
 FT DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 18 35 TNFR-CYS (PARTIAL).
 FT DISULFID 19 32 BY SIMILARITY.
 FT DISULFID 24 35 BY SIMILARITY.
 FT VARSPLIC 143 143 P -> PA (in isoform 2).
 FT /FTId=VSP_006505.
 SQ SEQUENCE 184 AA; 18863 MW; F2BFB98099A27138 CRC64;

Query Match 9.6%; Score 93; DB 1; Length 184;
 Best Local Similarity 26.5%; Pred. No. 0.12;
 Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCQL-----RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL 56
 | | | | : | : | | | | | : |
 Db 19 CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGLL 78
 Qy 57 W---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS 107
 : |||:|::| : | : || || | | : |
 Db 79 FGAPALLGLALVLALVLVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL----- 127
 Qy 108 RTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTTK 160
 |::| : | : : | || : | | :| | | |
 Db 128 ---DKVII---LSPGISDATAPAWPPPGEDPGTTPP----GHSVPVPATELGSTELVTTK 177
 Qy 161 T 161
 |
 Db 178 T 178

RESULT 6

PML1_MOUSE

ID PML1_MOUSE STANDARD; PRT; 867 AA.
AC O54990; O35408;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prominin 1 precursor (Prominin-like protein 1) (Antigen AC133
DE homolog).
GN PROM1 OR PROML1 OR PROM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Miraglia S., Godfrey W., Buck D.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98024147; PubMed=9356465;
RA Weigmann A., Corbeil D., Hellwig A., Huttner W.B.;
RT "Prominin, a novel microvilli-specific polytopic membrane protein of
RT the apical surface of epithelial cells, is targeted to plasmalemmal
RT protrusions of non-epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: In the embryo, expressed on the apical side of
CC neuroepithelial cells and of other epithelia such as lung buds,
CC gut and urether buds. In the adult, expressed at the apical side
CC of the kidney tubules and of the ependymal layer of the brain. Not
CC expressed in gut, liver, lung, pituitary, adrenal, heart or
CC spleen.
CC -!- SIMILARITY: Belongs to the prominin family.

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DR EMBL; AF039663; AAB96916.1; -.
DR EMBL; AF026269; AAB86715.1; -.
DR PIR; T08881; T08881.
DR MGD; MGI:1100886; Prom1.
DR GO; GO:0005903; C:brush border; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005902; C:microvillus; IDA.
DR InterPro; IPR008795; Prominin.
DR Pfam; PF05478; Prominin; 1.
KW Signal; Transmembrane; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 867 PROMININ 1.
FT DOMAIN 20 107 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	108	128	POTENTIAL.
FT	DOMAIN	129	158	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	159	179	POTENTIAL.
FT	DOMAIN	180	434	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	435	455	POTENTIAL.
FT	DOMAIN	456	487	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	488	508	POTENTIAL.
FT	DOMAIN	509	794	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	795	815	POTENTIAL.
FT	DOMAIN	816	867	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	273	273	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	374	374	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	415	415	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	554	554	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	581	581	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	732	732	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	64	64	S -> N (IN REF. 2).
FT	CONFLICT	84	84	K -> N (IN REF. 2).
FT	CONFLICT	94	102	MISSING (IN REF. 2).
FT	CONFLICT	668	668	P -> L (IN REF. 2).
FT	CONFLICT	844	844	G -> D (IN REF. 2).
SQ	SEQUENCE	867 AA;	97112 MW;	D442F6372552B3C8 CRC64;

Qy	18	LHACIPCQLRCSSTPPLTCQRYCNASVTNSVKGTNAILWTCGLSLIISLAVFVLMFLL	77
		: : : : :	
Db	126	LVGCFFCMCRC-----CNK-CGGEMHQ R Q K Q N A P C R R K C L G S L L V I C L L M S L G I I Y	176
Qy	78	RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE----	129
		: :: : : : : : :	
Db	177	GFVANQQTRTRI KGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTN TNKA	227
Qy	130	----DCIKS-----KPKVDSDHC FPLPAMEEGATILVTTK-TNDYCKSLPAAL--	172
		: : : : : :	
Db	228	FSDL DGI GSVLGGR IKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS	280
Qy	173	---SATEIEKSISA	183
		: : : : : :	
Db	281	LODAATOINTNLSS	294

GN PTK2B OR FAK2 OR PYK2 OR RAFTK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RT "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain.";
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [2]
 RP PTPNS1 BINDING.
 RX MEDLINE=99401000; PubMed=10469599;
 RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
 RA Schraven B., Neel B.G.;
 RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
 RT multi-protein complexes in macrophages.";
 RL Curr. Biol. 9:927-930(1999).
 RN [3]
 RP PHOSPHORYLATION OF TYR-402; TYR-580 AND TYR-881.
 RX MEDLINE=21313779; PubMed=11420674;
 RA Nakamura K., Yano H., Schaefer E., Sabe H.;
 RT "Different modes and qualities of tyrosine phosphorylation of Fak and
 RT Pyk2 during epithelial-mesenchymal transdifferentiation and cell
 RT migration: analysis of specific phosphorylation events using
 RT site-directed antibodies.";
 RL Oncogene 20:2626-2635(2001).
 RN [4]
 RP PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; PubMed=11493697;
 RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -!- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Interacts with Crk-associated substrate (Cas), PTPNS1,
 CC Nephrocystin and GTPase regulator associated with FAK (Graf).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase.
 CC -!- PTM: Phosphorylated on tyrosine residues in response to various
 CC stimuli that elevate the intracellular calcium concentration, as
 CC well as by PKC activation. Recruitment by Nephrocystin to cell
 CC matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,

CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 FERM domain.
 DR HSSP; P08631; 1AD5.
 DR MGD; MGI:104908; Ptk2b.
 DR InterPro; IPR000299; Band_4.1.
 DR InterPro; IPR005189; Focal_AT.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF03623; Focal_AT; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00660; FERM_1; FALSE_NEG.
 DR PROSITE; PS00661; FERM_2; FALSE_NEG.
 DR PROSITE; PS50057; FERM_3; 1.
 KW Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation.
 FT DOMAIN 39 359 FERM.
 FT DOMAIN 425 683 PROTEIN_KINASE.
 FT NP_BIND 431 439 ATP (BY SIMILARITY).
 FT BINDING 457 457 ATP (BY SIMILARITY).
 FT ACT_SITE 549 549 BY SIMILARITY.
 FT DOMAIN 701 767 PRO-RICH.
 FT DOMAIN 831 869 PRO-RICH.
 FT DOMAIN 868 1009 FOCAL ADHESION TARGETING (FAT).
 FT MOD_RES 402 402 PHOSPHORYLATION.
 FT MOD_RES 579 579 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 580 580 PHOSPHORYLATION.
 FT MOD_RES 881 881 PHOSPHORYLATION.
 SQ SEQUENCE 1009 AA; 115821 MW; 963959FF56DF9605 CRC64;

Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 7.9;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

Qy 88 EFKN TGSGLLGMANIDLEKSR-----TGDEIILPRGLE YTV EECTCEDCIKSKPKV 138
 :| || | | ||| | | | :| |:| : | | : :
 Db 249 KFFNT---LAGFANIDQET YRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
 Qy 139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
 | | || : ||| :: ||: ||:
 Db 306 RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSSLAEENMADLIDGYCR 353

RESULT 8
 FAK2_RAT
 ID FAK2_RAT STANDARD; PRT; 1009 AA.

AC P70600; O88489; Q63201;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 DE 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 DE beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
 GN PTK2B OR FAK2 OR PYK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE=Liver epithelium;
 RX MEDLINE=97094711; PubMed=8939945;
 RA Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 RA Wilm M., Anderegg R.J., Graves L.M., Earp H.S.;
 RT "Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 RT protein kinase activation.";
 RL J. Biol. Chem. 271:29993-29998(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95403356; PubMed=7673154;
 RA Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
 RP DOMAIN.
 RC TISSUE=Hippocampus;
 RX MEDLINE=98311659; PubMed=9645946;
 RA Xiong W.-C., Macklem M., Parsons J.T.;
 RT "Expression and characterization of splice variants of PYK2, a focal
 RT adhesion kinase-related protein.";
 RL J. Cell Sci. 111:1981-1991(1998).
 CC -!- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Interacts with PTPNS1 (By similarity). Isoform 1, but not
 CC isoform 2, interacts with Crk-associated substrate (Cas),
 CC Nephrocystin and GTPase regulator associated with FAK (Graf).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase (By similarity).
 CC Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.

```

CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1;
CC      IsoId=P70600-1; Sequence=Displayed;
CC      Name=2; Synonyms=PRNK;
CC      IsoId=P70600-2; Sequence=VSP_004982, VSP_004983;
CC      Name=3; Synonyms=PYK2s;
CC      IsoId=P70600-3; Sequence=VSP_004984;
CC  -!- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
CC      brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
CC      in the spleen and other tissues, whereas isoforms 2 and 3 are
CC      expressed in the spleen and brain (highest in cerebellum).
CC  -!- PTM: Phosphorylated on tyrosine residues in response to various
CC      stimuli that elevate the intracellular calcium concentration, as
CC      well as by PKC activation. Recruitment by Nephrocystin to cell
CC      matrix adhesions initiates Tyr-402 phosphorylation (By
CC      similarity). In monocytes, adherence to substrata is required for
CC      tyrosine phosphorylation and kinase activation. Angiotensin II,
CC      thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
CC      autophosphorylation and increase kinase activity.
CC  -!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
CC      subfamily.
CC  -!- SIMILARITY: Contains 1 FERM domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U69109; AAC52895.1; -.
DR  EMBL; D45854; BAA08290.1; -.
DR  EMBL; AF063890; AAC28340.1; -.
DR  PIR; A57434; A57434.
DR  HSSP; P00523; 2PTK.
DR  InterPro; IPR000299; Band_4.1.
DR  InterPro; IPR005189; Focal_AT.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  InterPro; IPR008266; Tyr_pkinase_AS.
DR  Pfam; PF03623; Focal_AT; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00295; B41; 1.
DR  SMART; SM00219; TyrKc; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR  PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00660; FERM_1; FALSE_NEG.
DR  PROSITE; PS00661; FERM_2; FALSE_NEG.
DR  PROSITE; PS50057; FERM_3; 1.
KW  Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
KW  Alternative splicing.
FT  DOMAIN          39      359      FERM.

```


FT	DOMAIN	425	683	PROTEIN KINASE.
FT	NP_BIND	431	439	ATP (BY SIMILARITY).
FT	BINDING	457	457	ATP (BY SIMILARITY).
FT	ACT_SITE	549	549	BY SIMILARITY.
FT	DOMAIN	701	767	PRO-RICH.
FT	DOMAIN	831	869	PRO-RICH.
FT	DOMAIN	868	1009	FOCAL ADHESION TARGETING (FAT).
FT	MOD_RES	402	402	PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	579	579	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	580	580	PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	881	881	PHOSPHORYLATION (BY SIMILARITY).
FT	VARSPLIC	1	771	Missing (in isoform 2).
FT				/FTId=VSP_004982.
FT	VARSPLIC	772	780	NVEKRHSMT -> MGLIVLSSQ (in isoform 2).
FT				/FTId=VSP_004983.
FT	VARSPLIC	739	780	Missing (in isoform 3).
FT				/FTId=VSP_004984.
FT	CONFLICT	205	205	E -> A (IN REF. 2).
FT	CONFLICT	807	807	V -> F (IN REF. 3).
SQ	SEQUENCE	1009 AA;	115784 MW;	D435A475BCA49E9B CRC64;

Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 7.9;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

Qy	88	EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV	138
		: : : : : ::	
Db	249	KFFNT---LAGFANIDQETRYCELIQGWNTVDLVIGPKGIRQLTSQDTPKTCLEAFKQI	305
Qy	139	DSDHCFPLPAME-----EGATILVTTKTND-----YCK	166
		: :: : :	
Db	306	RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEENMADLIDGYCR	353

RESULT 9

FAK2_HUMAN

ID FAK2_HUMAN STANDARD; PRT; 1009 AA.
 AC Q14289; Q13475; Q14290; Q16709;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
 adhesion focal tyrosine kinase).
 GN PTK2B OR FAK2 OR PYK2 OR RAFTK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=95379967; PubMed=7544443;
 RA Lev S., Moreno H., Martinez R., Canoll P., Peles E., Musacchio J.M.,
 RA Plowman G.D., Rudy B., Schlessinger J.;
 RT "Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation

RT of ion channel and MAP kinase functions.";
 RL Nature 376:737-745(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=96435932; PubMed=8838818;
 RA Herzog H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
 RT "Molecular cloning and assignment of FAK2, a novel human focal
 RT adhesion kinase, to 8p11.2-p22 by nonisotopic in situ hybridization.";
 RL Genomics 32:484-486(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=95403356; PubMed=7673154;
 RA Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RT "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain.";
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Monocytes;
 RX MEDLINE=98211954; PubMed=9545257;
 RA Li X., Hunter D., Morris J., Haskill J.S., Earp H.S.;
 RT "A calcium-dependent tyrosine kinase splice variant in human
 RT monocytes. Activation by a two-stage process involving adherence and a
 RT subsequent intracellular signal.";
 RL J. Biol. Chem. 273:9361-9364(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N.,
 RA Menzel U., Schilhabel M.B., Wen G., Taudien S., Rosenthal A.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP PHOSPHORYLATION OF TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
 RP WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; PubMed=11493697;
 RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -!- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kvl.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Interacts with Crk-associated substrate (Cas), PTPNS1 (By
 CC similarity), Nephrocystin and GTPase regulator associated with FAK
 CC (Graf).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q14289-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q14289-2; Sequence=VSP_004981;
 CC -!- TISSUE SPECIFICITY: Most abundant in the brain, with highest
 CC levels in amygdala and hippocampus. Low levels in kidney. Also
 CC expressed in spleen and lymphocytes.
 CC -!- PTM: Phosphorylated on tyrosine residues in response to various
 CC stimuli that elevate the intracellular calcium concentration, as
 CC well as by PKC activation. Recruitment by Nephrocystin to cell
 CC matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 FERM domain.

CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U33284; AAC50203.1; -.
DR EMBL; L49207; AAB47217.1; -.
DR EMBL; D45853; BAA08289.1; -.
DR EMBL; U43522; AAC05330.1; -.
DR EMBL; S80542; AAB35701.1; -.
DR EMBL; AF311103; -; NOT_ANNOTATED_CDS.
DR EMBL; BC042599; AAH42599.1; -.
DR PIR; S60248; S60248.
DR HSSP; P08631; 1AD5.
DR Genew; HGNC:9612; PTK2B.
DR MIM; 601212; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0004717; F:focal adhesion kinase activity; TAS.
DR GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. . .; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR GO; GO:0007172; P:signal complex formation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR005189; Focal_AT.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF03623; Focal_AT; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS50057; FERM_3; 1.
KW Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
KW Alternative splicing.
FT DOMAIN 39 359 FERM.
FT DOMAIN 425 683 PROTEIN KINASE.
FT NP_BIND 431 439 ATP (BY SIMILARITY).
FT BINDING 457 457 ATP (BY SIMILARITY).
FT ACT_SITE 549 549 BY SIMILARITY.
FT DOMAIN 702 767 PRO-RICH.
FT DOMAIN 831 869 PRO-RICH.
FT DOMAIN 868 1009 FOCAL ADHESION TARGETING (FAT).
FT MOD_RES 402 402 PHOSPHORYLATION.
FT MOD_RES 579 579 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 580 580 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 881 881 PHOSPHORYLATION (BY SIMILARITY).
FT VARSPLIC 739 780 Missing (in isoform 2).
FT /FTId=VSP_004981.

FT MUTAGEN 859 859 P->A: LOSS OF INTERACTION WITH
 FT NEPHROCYSTIN.
 FT CONFLICT 23 23 A -> G (IN REF. 3).
 FT CONFLICT 256 256 G -> P (IN REF. 2).
 FT CONFLICT 435 435 F -> L (IN REF. 3).
 FT CONFLICT 780 780 R -> G (IN REF. 2).
 SQ SEQUENCE 1009 AA; 115874 MW; 420B21046274E7C2 CRC64;

Query Match 8.2%; Score 79.5; DB 1; Length 1009;
 Best Local Similarity 32.1%; Pred. No. 13;
 Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

Qy 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEITYVEECTCEDCIKSKPKV 138
 :| || | | ||| | | | | :| | : : | : :
 Db 249 KFFNT---LAGFANIDQETRYCELIQGNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305

 Qy 139 DSDHCFPLPAMEEGATIL 156
 | | || || :|
 Db 306 RSIRCLPL---EEGQAVL 320

RESULT 10

T13X_HUMAN

ID T13X_HUMAN STANDARD; PRT; 293 AA.
 AC O14836;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TACI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; PubMed=9311921;
 RA von Buelow G.-U., Bram R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily.";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20519647; PubMed=10956646;
 RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
 RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., LaFleur D.,
 RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
 RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
 RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
 RT high affinity receptor for TNF family members APRIL and BlyS.";
 RL J. Biol. Chem. 275:35478-35485(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [5]
 RP INTERACTION WITH TRAF2 AND TRAF5.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.Y., Boyle W.J., Hsu H.;
 RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143(2000).
 CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity.
 CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus.
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
 CC intestine and peripheral blood leukocytes. Expressed in resting B-
 CC cells and activated T-cells, but not in resting T-cells.
 CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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CC -----

DR EMBL; AF023614; AAC51790.1; -.
DR EMBL; BC028072; AAH28072.1; -.
DR Genew; HGNC:18153; TNFRSF13B.
DR MIM; 604907; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 67 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 8.1%; Score 78.5; DB 1; Length 293;
Best Local Similarity 19.9%; Pred. No. 4.5;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

Qy 8 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
| : : | : | | : : | : : : | : : | : : |
Db 34 CP EEQYWDPLLGT C M SCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLRLDCISCASI 92

Qy 66 I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
| | | | : | : : | : | : : | |
Db 93 CGQHPKQ CAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151

Qy 108 ---RTGDEIILPRG-----LEYTVEECTCEDCIKSKP-----KVD 139
: | : : | : : : | : : : | : : |
Db 152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209

Qy 140 SDHCFPLPAMEEGATILVTTKTNDYC 165
| | | | : : : : : |
Db 210 QDH-----AMEAGSPVSTSPPEPVETC 230

RESULT 11

MJK2_METJA

ID MJK2_METJA STANDARD; PRT; 343 AA.

AC Q58752;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable potassium channel protein 2 (MjK2).
 GN MJ1357.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 RN [2]
 RP FUNCTION.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=22744766; PubMed=12860407;
 RA Hellmer J., Zeilinger C.;
 RT "MjK1, a K⁺ channel from M. jannaschii, mediates K⁺ uptake and K⁺
 RT sensitivity in E. coli.";
 RL FEBS Lett. 547:165-169(2003).
 CC -!- FUNCTION: Probable potassium channel protein.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- SIMILARITY: Contains 1 trkA/RCK domain.
 CC -----
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 CC -----
 DR EMBL; U67575; AAB99365.1; -.
 DR PIR; D64469; D64469.
 DR HSSP; Q54397; 1BL8.
 DR TIGR; MJ1357; -.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003148; TrkA_N.
 DR InterPro; IPR006037; TrkAC.
 DR Pfam; PF02080; TrkA-C; 1.
 DR Pfam; PF02254; TrkA-N; 1.
 KW Transport; Ion transport; Ionic channel; Potassium channel; Potassium;
 KW Potassium transport; Transmembrane; Complete proteome.
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 8 28 POTENTIAL.

Query Match 8.1%; Score 78.5; DB 1; Length 343;
Best Local Similarity 20.4%; Pred. No. 5.3;
Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;

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Qy      12 EYFDSLHLHACIPQLRCSSNTFPPLTCQRYCNASVTNSVKGTNAILWTCGLSLIISLAVF 71  
        :|| :| :|           :| | : :   : | ::: |:|: ::: |  
Db      32 DYFTALYFSVI-----TITTTGYGDFTPDKTFLGRTLTVVYLCSVGVGIVMYLFSL 80  
  
Qy      72 VLMFL-----LRKISS--EPLKDEFKNTGSGLLGMA-----NIDLEKSRTGD 111  
        : | :          |:|: : : ||| :   || ||         ||       :  
Db      81 IAEFIVEGKFEEFVRLKKMKMKNIKITLKDHYIICGYGR LGKVVG EK FIEENIPFIAIDINE 140  
  
Qy     112 EII-----LPRGLEYTVEECTCEDCIKSKPKV-----DSDHCF-PLPAMEEG 152  
        :::          |    || :   |: :| || :          |:|: |   || |  
Db     141 DVLKEEYEKYDPDKFLYIVGDAKKEEV LK-KAKIDKAKGLIATLP SADNVFLT LTARELN 199  
  
Qy     153 ATILVTTKTND 163  
        ||:| | ::  
Db     200 PNILITAKADE 210
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ID      T13X MOUSE          STANDARD;          PRT;    249 AA.
AC      Q9ET35; Q9DBZ3;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE      activator and CAML interactor).
GN      TNFRSF13B OR TACI.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RX      MEDLINE=21177254; PubMed=10881172;
RA      Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
RA      Dixit V.M.;
RT      "Identification of a receptor for BLyS demonstrates a crucial role in
RT      humoral immunity.";
RL      Nat. Immunol. 1:37-41(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Lung;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP FUNCTION.

RX MEDLINE=20341628; PubMed=10880535;

RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Hsu H.;

RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";

RL J. Exp. Med. 192:137-143(2000).

RN [4]

RP FUNCTION.

RX MEDLINE=21322748; PubMed=11429548;

RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;

RT "TACI-ligand interactions are required for T cell activation and
RT collagen-induced arthritis in mice.";

RL Nat. Immunol. 2:632-637(2001).

CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity (By
CC similarity).

CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus (By similarity).

CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.

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CC -----

DR EMBL; AF257673; AAG00081.1; -.

DR EMBL; AK004668; BAB23457.1; -.

DR MGD; MGI:1889411; Tnfrsf13b.

DR GO; GO:0005887; C:integral to plasma membrane; IDA.

RA Kueffner R., Rohr A., Schmiede A., Kruell C., Schulte U.;
 RT "Involvement of two novel chaperones in the assembly of mitochondrial
 RT NADH:ubiquinone oxidoreductase (complex 1).";
 RL J. Mol. Biol. 283:409-417(1998).
 CC -!- FUNCTION: Chaperone protein involved in the assembly of the
 CC mitochondrial NADH:ubiquinone oxidoreductase complex (complex I).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -----
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 CC -----
 DR EMBL; AJ001712; CAA04945.1; -.
 DR PIR; T47250; T47250.
 DR InterPro; IPR008941; TPR-like.
 KW Chaperone; Mitochondrion; Transit peptide.
 FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
 FT CHAIN 21 748 COMPLEX I INTERMEDIATE-ASSOCIATED
 FT PROTEIN 84.
 SQ SEQUENCE 748 AA; 86342 MW; 8B2D80E98E8CDC73 CRC64;

Query Match 7.9%; Score 76; DB 1; Length 748;
 Best Local Similarity 25.5%; Pred. No. 21;
 Matches 27; Conservative 20; Mismatches 49; Indels 10; Gaps 2;

Qy 82 SEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDS 141
 |:: | || || : | : | : | | : | : |
 Db 266 SKPIHSGFSPTGETLLELVRSSRRSSQKWNWLLP-----VFEQVVQDKFAKKGSLDAF 319
 Qy 142 HCFPLPAMEEG----ATILVTTKTNDYCKSLPAALSATEIEKSISA 183
 : : |:: | | | : | : | : | : | : | : |
 Db 320 LQWSVLALDKGPDGIKTYLQTMASGDFYQSHEVKVDATTINRLMQA 365

RESULT 14

YCSB_SCHPO

ID YCSB_SCHPO STANDARD; PRT; 638 AA.
 AC 074910;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical WD-repeat protein C613.12c in chromosome III.
 GN SPCC613.12C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RL Nature 415:871-880(2002).
 CC -!- SIMILARITY: Contains 4 WD repeats.
 CC -----
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 CC -----
 DR EMBL; AL031644; CAA21064.1; -.
 DR PIR; T41478; T41478.
 DR GeneDB_SPombe; SPCC613.12c; -.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 4.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR SMART; SM00320; WD40; 5.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS50082; WD_REPEATS_2; 2.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 297 336 WD 1.
 FT REPEAT 486 525 WD 2.
 FT REPEAT 544 583 WD 3.
 FT REPEAT 587 626 WD 4.
 SQ SEQUENCE 638 AA; 71536 MW; 6CD360D8748AAF98 CRC64;

Query Match 7.8%; Score 75.5; DB 1; Length 638;
 Best Local Similarity 22.7%; Pred. No. 20;
 Matches 44; Conservative 20; Mismatches 61; Indels 69; Gaps 7;

Qy 12 EYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVF 71

```

      | :|   | :||   | | :  :: | | : :|   | | | : :  |
Db      42 EIYDPFYRAELPCP-----KPSLSISKHSIAKVPSNVNKR-----LELQLLLTSGTF 88

Qy      72 VLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC----- 126
      :      :| |   |   : |   | | | | :      : :| | |
Db      89 L-----PNSRPYLSERVVRKHTHL-----LSNSITGDDKPSLIHVDFTPPEECFILQE 134

Qy      127 -----TCEDCIKSKPKVDSHCFPLPAMEEGATILVT 158
      |||   | : | :   | : || | | |
Db      135 AKLKFGPVNSVQFNDAYSTHISPKLPGRAYEDC----QKFEIDNPSLSPVDKHGAILRT 190

Qy      159 TKTN-----DYCKS 167
      | |   || | |
Db      191 YKKNKKLLPDYLS 204

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RESULT 15

SRK6_BRAOL

```

ID   SRK6_BRAOL          STANDARD;          PRT;   849 AA.
AC   Q09092;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
DE   (S-receptor kinase) (SRK).
GN   SRK6.
OS   Brassica oleracea (Cauliflower).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3712;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. S6S6; TISSUE=Stigma;
RX   MEDLINE=92020942; PubMed=1681543;
RA   Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;
RT   "Molecular cloning of a putative receptor protein kinase gene encoded
RT   at the self-incompatibility locus of Brassica oleracea.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).
CC   -!- FUNCTION: Involved in sporophytic self-incompatibility system
CC   (the inability of flowering plants to achieve self-
CC   fertilization), probably acting in combination with S-locus-
CC   specific glycoproteins. Interaction with a ligand in the
CC   extracellular domain triggers the protein kinase activity of the
CC   cytoplasmic domain.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Predominantly in the pistil and anther.
CC   -!- POLYMORPHISM: There are a number of different S alleles in
CC   B.oleracea, possibly providing the recognition specificity.
CC   -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC   -!- SIMILARITY: Contains 1 bulb-type lectin domain.
CC   -!- SIMILARITY: Contains 1 PAN domain.

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CC   -----
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M76647; AAA33000.1; ALT_TERM.
 DR InterPro; IPR001480; B_lectin.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR000858; Slocus_glycop.
 DR Pfam; PF01453; Agglutinin; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00954; S_locus_glycop; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00108; B_lectin; 1.
 DR SMART; SM00473; PAN_AP; 1.
 DR PROSITE; PS50927; BULB_LLECTIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Signal; ATP-binding;
 KW Transmembrane; Receptor; Glycoprotein; Self-incompatibility.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 849 PUTATIVE SERINE/THREONINE KINASE
 FT RECEPTOR.
 FT DOMAIN 33 446 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 447 466 POTENTIAL.
 FT DOMAIN 467 849 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 35 155 BULB-TYPE LECTIN.
 FT DOMAIN 528 779 PROTEIN KINASE.
 FT NP_BIND 534 542 ATP (BY SIMILARITY).
 FT BINDING 556 556 ATP (BY SIMILARITY).
 FT ACT_SITE 653 653 BY SIMILARITY.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 849 AA; 97231 MW; 7E156059EDDF4370 CRC64;

Query Match 7.8%; Score 75; DB 1; Length 849;
 Best Local Similarity 17.6%; Pred. No. 30;
 Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

Qy 24 CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT----- 58
 | : || | : | : || : | | : : ||
 Db 380 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTTERLEDIRNYATDAIDGQDLYVRLAA 434
 Qy 59 -----CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
 : | : : | : : || | | : | : : || :
 Db 435 ADIAKKRNASGKIISLTVGVSVLLLLLIMFCL-----WKRKQKRAKASAI SIANTQRNQ 487
 Qy 107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSHCF----PLPAMEEGATILVTTKT 161
 : : || : | | : : | | | | : : | :

Db 488 NLPNMNEMVL-----SSKREFSGEYKFEELELPLIEME---TVVKATEN 527
Qy 162 NDYCKSL 168
| |
Db 528 FSSCNKL 534

Search completed: April 19, 2004, 13:21:30
Job time : 9.57202 secs